

SEQUENCE LISTING

<110> Koffas, Mattheos
Odom, James M
Schenzle, Andreas J

<120> DENITRIFYING METHANOTROPHIC BACTERIAL STRAIN

<130> CL1596 US NA

<140>
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<150> 60/229,858
<151> September 1, 2000

<160> 81

<170> Microsoft Office 97

<210> 1
<211> 1434
<212> DNA
<213> METHYLOMONAS SP.

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tccattttca atagtttaga agatttcag gaaaaattc tagttttagg cggcgacggc 180
cgatatttta atcgacaagg gattcagatc atcatcaaaa tggccggccgc taacgggtt 240
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cgcaaataatc gcgcatttcgg cgccatcatt ctatccgcca gccacaatcc cggtggtccc 360
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accgacgcct tgttcgaaaa cagcaaaaacc atcaccagct atcagatggc cggaaatcgac 480
gacatcgatc tcgatagcgt cggcgacgatc caaatcgatg gcataacaat cggcatcatc 540
gatccccgtgg ccgattacgc cgaattgatg gcccggattt tcgatttcga cctgatcaag 600
caaagcatcg cccggccgtt gattaccttgc cgcttcgacg cgatgcattgc cattaccggc 660
ccctatgcca aacatataact cgaagacgtg ctggggccgc cggccgggtt ggtattcaac 720
gccgtaccgc tggaaagactt cggcgccggc catcccgatc ccaacatggc gcacgcgcac 780
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gccgtcgatg cgcacatcgca acacggcatc gttaggcgc tgcaaaacca attgccgagc 1320
ttggccggca aaacctgggg cgattacagc gtcaaattcg cgcacgaatt cagctataacc 1380
gatccggtcg atggtagcgt cagcagcaac caaggcatcc cggtcggtt cgcc 1434

<210> 2
<211> 545
<212> PRT
<213> METHYLOMONAS SP.

<400> 2
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Pro Gly Thr Ser Gly Leu Arg Lys Lys Val Lys Val Phe Gln Gln Ser
 20 25 30

 Gly Tyr Leu Glu Asn Phe Val Gln Ser Ile Phe Asn Ser Leu Glu Asp
 35 40 45

 Phe Gln Gly Lys Ile Leu Val Leu Gly Gly Asp Gly Arg Tyr Phe Asn
 50 55 60

 Arg Gln Ala Ile Gln Ile Ile Lys Met Ala Ala Ala Asn Gly Phe
 65 70 75 80

 Gly Glu Leu Ile Ile Gly Gln Gly Leu Leu Ser Thr Pro Ala Ala
 85 90 95

 Ser Asn Val Ile Arg Lys Tyr Arg Ala Phe Gly Gly Ile Ile Leu Ser
 100 105 110

 Ala Ser His Asn Pro Gly Gly Pro Asp Glu Asp Phe Gly Ile Lys Tyr
 115 120 125

 Asn Val Gly Asn Gly Gly Pro Ala Pro Glu Lys Phe Thr Asp Ala Leu
 130 135 140

 Phe Glu Asn Ser Lys Thr Ile Thr Ser Tyr Gln Met Ala Glu Ile Asp
 145 150 155 160

 Asp Ile Asp Leu Asp Ser Val Gly Asp Val Gln Ile Asp Gly Ile Thr
 165 170 175

 Ile Arg Ile Ile Asp Pro Val Ala Asp Tyr Ala Glu Leu Met Ala Arg
 180 185 190

 Ile Phe Asp Phe Asp Leu Ile Lys Gln Ser Ile Ala Ala Gly Leu Ile
 195 200 205

 Thr Leu Arg Phe Asp Ala Met His Ala Ile Thr Gly Pro Tyr Ala Lys
 210 215 220

 His Ile Leu Glu Asp Val Leu Gly Ala Ala Pro Gly Ser Val Phe Asn
 225 230 235 240

 Ala Val Pro Leu Glu Asp Phe Gly Gly His Pro Asp Pro Asn Met
 245 250 255

 Ala His Ala His Glu Leu Thr Glu Ile Met Phe Gly Pro Asn Pro Pro
 260 265 270

 Val Phe Gly Ala Ala Ser Asp Gly Asp Gly Asp Arg Asn Met Ile Met
 275 280 285

 Gly Ala Asn Ile Phe Val Thr Pro Ser Asp Ser Leu Ala Ile Met Ala
 290 295 300

 Ala Asn Ala Gln Leu Ile Pro Ala Tyr Ala Lys Gly Ile Ser Gly Val
 305 310 315 320

 Ala Arg Ser Met Pro Thr Ser Gln Ala Val Asp Arg Val Ala Asp Lys
 325 330 335

Leu Ser Leu Pro Cys Tyr Glu Thr Pro Thr Gly Trp Lys Phe Phe Gly
 340 345 350
 Asn Leu Leu Asp Ala Asp Lys Ile Thr Leu Cys Gly Glu Glu Ser Phe
 355 360 365
 Gly Ser Gly Ser Asn His Val Arg Glu Lys Asp Gly Leu Trp Ala Val
 370 375 380
 Leu Phe Trp Leu Asn Leu Leu Ala Arg Lys Arg Gln Pro Ala Glu Asp
 385 390 395 400
 Ile Val Arg Glu His Trp Gln Lys Tyr Gly Arg Asp Ile Tyr Cys Arg
 405 410 415
 His Asp Tyr Glu Ala Val Asp Ala Asp Ile Ala Asn Gly Ile Val Glu
 420 425 430
 Gln Leu Arg Asn Gln Leu Pro Ser Leu Pro Gly Lys Thr Trp Gly Asp
 435 440 445
 Tyr Ser Val Lys Phe Ala Asp Glu Phe Ser Tyr Thr Asp Pro Val Asp
 450 455 460
 Gly Ser Val Ser Ser Asn Gln Gly Ile Arg Val Gly Phe Ala Asn Gly
 465 470 475 480
 Ser Arg Ile Val Phe Arg Leu Ser Gly Thr Gly Thr Val Gly Ala Thr
 485 490 495
 Leu Arg Ile Tyr Leu Glu Arg Tyr Glu Arg Asp Val Arg Asn His Asp
 500 505 510
 Gln Asp Pro Gln Val Ala Leu Ala Glu Leu Ile Glu Ile Ala Glu Gln
 515 520 525
 Leu Cys Gln Val Lys Gln Arg Thr Gly Arg Thr Glu Pro Ser Val Ile
 530 535 540

Thr
 545

<210> 3
 <211> 1387
 <212> DNA
 <213> METHYLOMONAS SP.

<400> 3
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 ggttcacaca aaaataatat gtccaaatta atcaactctg ccgaatggaa cgccgtcaaa 180
 caacatcatc aaaaaattgc tggtaaattt tgcatgaaag aggctttgc caaagatccc 240
 cagcgttcg ataaattctc cgtcacctt aacgacatata tattagacta ttccaaaaaac 300
 ctgatcgacg agcgcaccat gcccattgctg atcgcattgg caaagcgggc agacttgccg 360
 gagaaaaacgg aagcgatgtt ttccggctcc atcatcaaca ccaccgaaaa acgcgcgggtt 420
 ttgcataaccg cgctgcgaaa cctgttagcaat acgccccgtt tctttccggcgg ccaggatgtc 480
 atgccggaaa tcaacaaggt tctggcaaaa atgcgggttt tcgtggaaca ggtgcgttcg 540
 ggccaatgga cggcgtatacg cggcaaggcc attaccgata tcgtcaacat cggcattggc 600

ggctcgatc	tcggccgaa	aatggtcgac	accgccttga	cggcgtacgg	caaaaacggc	660
ttaaaagcgc	atttcgtatc	caatgtcgat	caaaccgaca	tcgtcgaaac	cctgaaaccg	720
ctcaatccgg	aaaccacgct	gttcctgatt	tcatcgaaaa	cgttaccac	gcaggaaacc	780
atgaccaatg	cgcgctcgcc	acgtaactgg	ttcatgaatg	ccgcgcaaga	tcccggccat	840
atcaagaaac	atttcatcgc	catttccacc	aacgaagaaa	tggtcaagga	attcggcattc	900
gaccggcga	acatgttcga	gttctggac	tgggtcgccg	ggcgttattc	gctctggtcg	960
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ggtgccact	tggccgacga	acatttccgc	catgcgccct	acgaggaaaa	cattccggtc	1080
atcatggct	tgctcgcat	ctggtacaac	aacttcttcg	aagcgaaac	ctatgccatt	1140
ttgccgtatg	cgcaatcctt	gaaatattt	gccgattatt	tccagcaagg	cgacatggaa	1200
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atctggggac	agcccgac	caatggtcag	cacgccttct	ttcaattgtat	tcaccaaggc	1320
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caccacg						1387

<210> 4
<211> 592
<212> PRT
<213> METHYLOMONAS SP.

Asp Asn Pro Tyr Asn Glu Val Ile Val Leu Leu Ala Thr Ser Gly Thr					
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Lys Ala Ser Glu Asp Ser Leu Ser Gly Ser His Lys Asn Asn Met Ser					
35	40	45			
Lys Leu Ile Asn Ser Ala Glu Trp Asn Ala Val Lys Gln His His Gln					
50	55	60			
Glu Ile Ala Gly Lys Phe Cys Met Lys Glu Ala Phe Ala Lys Asp Pro					
65	70	75	80		
Gln Arg Phe Asp Lys Phe Ser Val Thr Phe Asn Asp Ile Leu Leu Asp					
85	90	95			
Tyr Ser Lys Asn Leu Ile Asp Glu Arg Thr Met Pro Leu Leu Ile Ala					
100	105	110			
Leu Ala Lys Arg Ala Asp Leu Arg Glu Lys Thr Glu Ala Met Phe Ser					
115	120	125			
Gly Ser Ile Ile Asn Thr Thr Glu Lys Arg Ala Val Leu His Thr Ala					
130	135	140			
Leu Arg Asn Arg Ser Asn Thr Pro Val Phe Phe Arg Gly Gln Asp Val					
145	150	155	160		
Met Pro Glu Ile Asn Lys Val Leu Ala Lys Met Arg Val Phe Val Glu					
165	170	175			
Gln Val Arg Ser Gly Gln Trp Thr Gly Tyr Ser Gly Lys Ala Ile Thr					
180	185	190			
Asp Ile Val Asn Ile Gly Ile Gly Ser Asp Leu Gly Pro Lys Met					
195	200	205			

Val Asp Thr Ala Leu Thr Pro Tyr Gly Lys Asn Gly Leu Lys Ala His
210 215 220

Phe Val Ser Asn Val Asp Gln Thr Asp Ile Val Glu Thr Leu Lys Pro
225 230 235 240

Leu Asn Pro Glu Thr Thr Leu Phe Leu Ile Ser Ser Lys Thr Phe Thr
245 250 255

Thr Gln Glu Thr Met Thr Asn Ala Arg Ser Ala Arg Asn Trp Phe Met
260 265 270

Asn Ala Ala Gln Asp Pro Ala His Ile Lys Lys His Phe Ile Ala Ile
275 280 285

Ser Thr Asn Glu Glu Met Val Lys Glu Phe Gly Ile Asp Pro Ala Asn
290 295 300

Met Phe Glu Phe Trp Asp Trp Val Gly Gly Arg Tyr Ser Leu Trp Ser
305 310 315 320

Val Ile Gly Met Ser Ile Ala Leu Tyr Ile Gly Met Asp Asn Phe Glu
325 330 335

Glu Leu Leu Met Gly Ala His Leu Ala Asp Glu His Phe Arg His Ala
340 345 350

Pro Tyr Glu Glu Asn Ile Pro Val Ile Met Gly Leu Leu Gly Ile Trp
355 360 365

Tyr Asn Asn Phe Phe Glu Ala Glu Thr Tyr Ala Ile Leu Pro Tyr Ala
370 375 380

Gln Ser Leu Lys Tyr Phe Ala Asp Tyr Phe Gln Gln Gly Asp Met Glu
385 390 395 400

Ser Asn Gly Lys Ser Ala Thr Ile Thr Gly Glu Lys Val Asp Tyr Asn
405 410 415

Thr Gly Pro Ile Ile Trp Gly Gln Pro Gly Thr Asn Gly Gln His Ala
420 425 430

Phe Phe Gln Leu Ile His Gln Gly Thr Lys Leu Val Pro Gly Asp Phe
435 440 445

Leu Ala Ala Ala Gln Ser Gln Tyr Asp Leu Pro Asp His His Asp Ile
450 455 460

Leu Ile Ser Asn Phe Leu Ala Gln Ala Glu Ala Leu Met Arg Gly Lys
465 470 475 480

Thr Glu Glu Glu Val Arg Gln Asp Leu Ser His Glu Pro Asn Leu Asp
485 490 495

Asp Ala Leu Ile Ala Ser Lys Ile Phe Glu Gly Asn Lys Pro Ser Asn
500 505 510

Ser Phe Leu Phe Lys Lys Leu Thr Pro Arg Thr Leu Gly Thr Leu Ile
515 520 525

Ala Phe Tyr Glu His Lys Ile Phe Val Gln Gly Val Ile Trp Asn Ile
530 535 540

Asn Ser Phe Asp Gln Met Gly Val Glu Leu Gly Lys Val Leu Ala Lys
545 550 555 560

Ala Ile Leu Pro Glu Leu Lys Asn Asp Asp Ile Ile Ala Ser His Asp
565 570 575

Ser Ser Thr Asn Gly Leu Ile Asn Thr Tyr Lys Arg Leu Arg Lys Ala
580 585 590

<210> 5

<211> 1311

<212> DNA

<213> METHYLOMONAS SP.

<400> 5

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atcgatctca gcatagaaaat catttgctat cgccggcggtt ataaaggcct gttgctggc 240
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gcagcattcc tggccagaaaa taattacgga ctgaccgtca ttggtttacc taaaaccgtc 540
gataacgacg tatttccgat caagcaatca cttaggtgctt ggactgcccgc cgagcaaggc 600
gcgcgttatt tcatgaacgt ggtggccgaa aacaacgcca acccacgcat gctgatcgta 660
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gagttccgc gcatcaaggg cggcaaaaccg ttcaatatcg acaccgactg gttcaatagc 1260
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<210> 6

<211> 437

<212> PRT

<213> METHYLOMONAS SP.

<400> 6

Asp Val Val Thr Trp Pro Tyr His Leu Thr Ala Asp Ile Arg Phe Cys
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His Trp Phe Phe Leu Asn Phe Asn Phe Tyr Thr Leu Met Asn Lys Pro
20 25 30

Lys Lys Val Ala Ile Leu Thr Ala Gly Gly Leu Ala Pro Cys Leu Asn
35 40 45

Ser Ala Ile Gly Ser Leu Ile Glu Arg Tyr Thr Glu Ile Asp Pro Ser
 50 55 60

Ile Glu Ile Ile Cys Tyr Arg Gly Gly Tyr Lys Gly Leu Leu Leu Gly
 65 70 75 80

Asp Ser Tyr Pro Val Thr Ala Glu Val Arg Lys Lys Ala Gly Val Leu
 85 90 95

Gln Arg Phe Gly Gly Ser Val Ile Gly Asn Ser Arg Val Lys Leu Thr
 100 105 110

Asn Val Lys Asp Cys Val Lys Arg Gly Leu Val Lys Glu Gly Glu Asp
 115 120 125

Pro Gln Lys Val Ala Ala Asp Gln Leu Val Lys Asp Gly Val Asp Ile
 130 135 140

Leu His Thr Ile Gly Gly Asp Asp Thr Asn Thr Ala Ala Ala Asp Leu
 145 150 155 160

Ala Ala Phe Leu Ala Arg Asn Asn Tyr Gly Leu Thr Val Ile Gly Leu
 165 170 175

Pro Lys Thr Val Asp Asn Asp Val Phe Pro Ile Lys Gln Ser Leu Gly
 180 185 190

Ala Trp Thr Ala Ala Glu Gln Gly Ala Arg Tyr Phe Met Asn Val Val
 195 200 205

Ala Glu Asn Asn Ala Asn Pro Arg Met Leu Ile Val His Glu Val Met
 210 215 220

Gly Arg Asn Cys Gly Trp Leu Thr Ala Ala Thr Ala Gln Glu Tyr Arg
 225 230 235 240

Lys Leu Leu Asp Arg Ala Glu Trp Leu Pro Glu Leu Gly Leu Thr Arg
 245 250 255

Glu Ser Tyr Glu Val His Ala Val Phe Val Pro Glu Met Ala Ile Asp
 260 265 270

Leu Glu Ala Glu Ala Lys Arg Leu Arg Glu Val Met Asp Lys Val Asp
 275 280 285

Cys Val Asn Ile Phe Val Ser Glu Gly Ala Gly Val Glu Ala Ile Val
 290 295 300

Ala Glu Met Gln Ala Lys Gly Gln Glu Val Pro Arg Asp Ala Phe Gly
 305 310 315 320

His Ile Lys Leu Asp Ala Val Asn Pro Gly Lys Trp Phe Gly Glu Gln
 325 330 335

Phe Ala Gln Met Ile Gly Ala Glu Lys Thr Leu Val Gln Lys Ser Gly
 340 345 350

Tyr Phe Ala Arg Ala Ser Ala Ser Asn Val Asp Asp Met Arg Leu Ile
 355 360 365

Lys Ser Cys Ala Asp Leu Ala Val Glu Cys Ala Phe Arg Arg Glu Ser
370 375 380

Gly Val Ile Gly His Asp Glu Asp Asn Gly Asn Val Leu Arg Ala Ile
385 390 395 400

Glu Phe Pro Arg Ile Lys Gly Lys Pro Phe Asn Ile Asp Thr Asp
405 410 415

Trp Phe Asn Ser Met Leu Ser Glu Ile Gly Gln Pro Lys Gly Gly Lys
420 425 430

Val Glu Val Ser His
435

<210> 7
<211> 1360
<212> DNA
<213> METHYLOMONAS SP.

<400> 7
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gccgcacatcg ccgaaggccc gcaacgcaat aaactgcctt ggcacatct ggcccacgg 180
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cccgcgatgt ggcacggcgt caccaggc atgcccggca tggattgtc gctattcagc 420
cgcgacgtca tcgcgatgtc caccgcgatc ggcctggctc ataacatgtt cgacgcgcg 480
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ggccatttgc cggccgtttt cttgccagcc ggccccatga ccagcggcct gtccaacaag 600
aaaaaatccc gtgcccggca aaaatacgcc gaaggtaaga tcggtaaaa agaattgtc 660
gaatcgaaag ccaagtctta ccacagccca ggcacctgca cttcttatgg caccgccaac 720
agcaaccaga tgcgttgcga gatcatggc ctgcacctgc cccgtatgc cttcatcaat 780
ccttacaccc cactgcgcga cgaactgacc aaggccgccc ccaggcaggt ttgaaattc 840
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gcggccggcg gcatgagctt attgatacac gaactgttgc atcacggctt gttgcacggc 1140
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caagacggcc aattacaatg gcaagccggc cttaccgcat cgcgcgatcc cggaaatcatc 1260
gccagcgtgg caaaacctt cggccgggt ggtggctgc atgtgatgca tggcaatctg 1320
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<210> 8
<211> 618
<212> PRT
<213> METHYLOMONAS SP.

<400> 8
Ser Val Pro His Ser His His Pro Glu Thr Ser Leu Met His Pro Val
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20 25 30

Ala Ala Tyr Leu Lys Arg Ile Glu Ala Ala Ile Ala Glu Gly Pro Gln
 35 40 45

 Arg Asn Lys Leu Pro Cys Ala Asn Leu Ala His Gly Phe Ala Val Cys
 50 55 60

 Ser Ala Ile Glu Lys Glu Glu Leu Ser His Gly Pro Lys Pro Asn Val
 65 70 75 80

 Gly Ile Ile Ser Ala Tyr Asn Asp Met Leu Ser Ala His Glu Pro Tyr
 85 90 95

 Lys Asp Tyr Pro Ala Leu Ile Lys Gln Ala Val Arg Glu Ala Gly Gly
 100 105 110

 Val Ala Gln Phe Ala Gly Gly Val Pro Ala Met Cys Asp Gly Val Thr
 115 120 125

 Gln Gly Met Pro Gly Met Glu Leu Ser Leu Phe Ser Arg Asp Val Ile
 130 135 140

 Ala Met Ser Thr Ala Ile Gly Leu Ala His Asn Met Phe Asp Ala Ala
 145 150 155 160

 Leu Tyr Leu Gly Val Cys Asp Lys Ile Val Pro Gly Leu Leu Ile Gly
 165 170 175

 Ala Leu Ser Phe Gly His Leu Pro Ala Val Phe Leu Pro Ala Gly Pro
 180 185 190

 Met Thr Ser Gly Leu Ser Asn Lys Glu Lys Ser Arg Ala Arg Gln Lys
 195 200 205

 Tyr Ala Glu Gly Lys Ile Gly Glu Lys Glu Leu Leu Glu Ser Glu Ala
 210 215 220

 Lys Ser Tyr His Ser Pro Gly Thr Cys Thr Phe Tyr Gly Thr Ala Asn
 225 230 235 240

 Ser Asn Gln Met Met Val Glu Ile Met Gly Leu His Leu Pro Gly Ser
 245 250 255

 Ser Phe Ile Asn Pro Tyr Thr Pro Leu Arg Asp Glu Leu Thr Lys Ala
 260 265 270

 Ala Ala Arg Gln Val Leu Lys Phe Thr Ala Leu Gly Asn Asp Phe Arg
 275 280 285

 Pro Ile Ala His Val Ile Asp Glu Lys Ala Ile Ile Asn Ala Ile Ile
 290 295 300

 Gly Leu Leu Ala Thr Gly Gly Ser Thr Asn His Thr Ile His Leu Ile
 305 310 315 320

 Ala Ile Ala Arg Ala Ala Gly Ile Ile Asn Trp Asp Asp Phe Asp
 325 330 335

 Ala Leu Ser Lys Val Ile Pro Leu Leu Thr Lys Ile Tyr Pro Asn Gly
 340 345 350

Pro Ala Asp Val Asn Gln Phe Gln Ala Ala Gly Gly Met Ser Leu Leu
 355 360 365

Ile His Glu Leu Leu Asp His Gly Leu Leu His Gly Asp Ile Leu Thr
 370 375 380

Ile Gly Asp Gln Arg Gly Met Ala Gln Tyr Ser Gln Val Pro Thr Leu
 385 390 395 400

Gln Asp Gly Gln Leu Gln Trp Gln Pro Gly Pro Thr Ala Ser Arg Asp
 405 410 415

Pro Glu Ile Ile Ala Ser Val Ala Lys Pro Phe Ala Ala Gly Gly Gly
 420 425 430

Leu His Val Met His Gly Asn Leu Gly Arg Gly Val Ser Lys Ile Ser
 435 440 445

Ala Val Ser Glu Asp His Gln Val Val Thr Ala Pro Ala Met Val Phe
 450 455 460

Asp Asp Gln Leu Asp Val Val Ala Ala Phe Lys Arg Gly Glu Leu Glu
 465 470 475 480

Lys Asp Val Ile Val Val Leu Arg Phe Gln Gly Pro Lys Ala Asn Gly
 485 490 495

Met Pro Glu Leu His Lys Leu Thr Pro Val Leu Gly Val Leu Gln Asp
 500 505 510

Arg Gly Phe Lys Val Gly Leu Leu Thr Asp Gly Arg Met Ser Gly Ala
 515 520 525

Ser Gly Lys Val Pro Ser Ala Ile His Met Trp Pro Glu Cys Ile Asp
 530 535 540

Gly Gly Pro Leu Ala Lys Val Arg Asp Gly Asp Ile Ile Val Met Asn
 545 550 555 560

Thr Gln Thr Gly Glu Val Asn Val Gln Val Asp Pro Ala Glu Phe Lys
 565 570 575

Ala Arg Val Ala Glu Pro Asn His Ala Thr Gly His His Phe Gly Met
 580 585 590

Gly Arg Glu Leu Phe Gly Ala Met Arg Ala Gln Ala Ser Thr Ala Glu
 595 600 605

Thr Gly Ala Thr Asn Leu Phe Phe Val Asp
 610 615

<210> 9
 <211> 1477
 <212> DNA
 <213> METHYLOMONAS SP.

<400> 9
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tcattatacc	gttggaaaa	acacaatctg	ctcgagcccg	atacgcgcac	catcgccgt	180
gatcgtttg	aagaaaccag	cgacagttc	gtcggaaattt	cgcacaaaag	cttgcaggcg	240
ttttgaaca	acgtcatcga	cgcagaaatc	tggcaacgtt	tttccaaacg	cttgcctat	300
ttgaaaatcg	atctgaccct	acccgagcaa	tacaaacaac	tgcatacgg	cgtcgatgcc	360
gaaaaacgag	tcatggtgaa	ttatttcgcg	gtggcaccc	ttttgttcaa	aaacatttc	420
caaggcttc	atgactgcgg	cgtattgacg	gccgaatcgc	gcatgggtat	ggaaaaaccc	480
atcggccacg	acctgaaatc	gtcgaaagaa	atcaacgcac	tcgtcgccga	cgtattccac	540
gaagaccagg	tctaccgcac	cgaccactac	ctgggcaagg	aaacggctt	gaacttgctg	600
gccttcgtt	tcgccaattc	gatattcag	accaactgga	atcacaacac	gatagaccat	660
atccagatta	cggcgggtga	ggacatcgac	atcgagggcc	gttggaaata	tttcgacaag	720
accggccaaat	tgcgcgacat	gtcgaaaac	catttgcgc	aaatcctgac	cttcgtcg	780
atggagccgc	ccgcggatct	gtcgccgaa	agcatacaca	tggaaaaat	caaggtctg	840
aaaggcttc	ggccaatcac	cgtgcgcaat	gtcgaggaaa	aaaccgtcg	cggtaatac	900
accggccgtt	tcatcaaagg	caagtgcgt	ccgggttatac	tggaagaaga	aggtgccaac	960
accgaaagca	cgaccgaaac	tttcgtcg	atccgcgtgg	atatcgataa	ctggcgctgg	1020
gccgggttcc	cgttttacat	cggtaccggc	aaacgcacgc	ccaacaaacg	caccgagatt	1080
gtggtaatt	tcaagcaatt	gccgcacaac	atcttcaagg	acagtttca	tgaactgccc	1140
gccaataaac	tggtcattca	tttgcaccc	aacgaagggg	tggatgtcat	gatgttgaac	1200
aagggtgcgg	gcatacgg	caacatcaag	ttgcaacaga	ccaaactgga	tttgagctt	1260
tccgaaacct	tcaagaaaaa	ccgaatttcc	ggcggtacg	aaaaactgat	tctggaaagcc	1320
ctgcgcggca	accgcacgt	gttttgagc	cgcgaggaaa	tagaacaagc	ctggacctgg	1380
gtcgattcga	ttaggatgc	ctggcaacac	aaccacacgc	cacccaaacc	ctatcccgc	1440
gttagctggg	gtccagtggc	atcggtcgca	ttactgg			1477

<210> 10

<211> 501

<212> PRT

<213> METHYLOMONAS SP.

<400> 10

Met	ala	Leu	Gly	Phe	Leu	Leu	Arg	Ser	Pro	Lys	Asp	Met	Thr	Lys	Asn
1				5					10			15			

Ile	Thr	Tyr	Lys	Pro	Cys	Asp	Leu	Val	Ile	Tyr	Gly	Ala	Leu	Gly	Asp
			20					25				30			

Leu	Ser	Lys	Arg	Lys	Leu	Leu	Ile	Ser	Leu	Tyr	Arg	Leu	Glu	Lys	His
				35				40				45			

Asn	Leu	Leu	Glu	Pro	Asp	Thr	Arg	Ile	Ile	Gly	Val	Asp	Arg	Leu	Glu
				50				55			60				

Glu	Thr	Ser	Asp	Ser	Phe	Val	Glu	Ile	Ala	His	Lys	Ser	Leu	Gln	Ala
				65				70			75			80	

Phe	Leu	Asn	Asn	Val	Ile	Asp	Ala	Glu	Ile	Trp	Gln	Arg	Phe	Ser	Lys
					85			90			95				

Arg	Leu	Ser	Tyr	Leu	Lys	Ile	Asp	Leu	Thr	Gln	Pro	Glu	Gln	Tyr	Lys
				100				105			110				

Gln	Leu	His	Thr	Val	Val	Asp	Ala	Glu	Lys	Arg	Val	Met	Val	Asn	Tyr
					115			120			125				

Phe	Ala	Val	Ala	Pro	Phe	Leu	Phe	Lys	Asn	Ile	Cys	Gln	Gly	Leu	His
					130			135			140				

Asp	Cys	Gly	Val	Leu	Thr	Ala	Glu	Ser	Arg	Met	Val	Met	Glu	Lys	Pro
				145				150			155			160	

Ile Gly His Asp Leu Lys Ser Ser Lys Glu Ile Asn Asp Val Val Ala
 165 170 175
 Asp Val Phe His Glu Asp Gln Val Tyr Arg Ile Asp His Tyr Leu Gly
 180 185 190
 Lys Glu Thr Val Leu Asn Leu Leu Ala Leu Arg Phe Ala Asn Ser Ile
 195 200 205
 Phe Thr Thr Asn Trp Asn His Asn Thr Ile Asp His Ile Gln Ile Thr
 210 215 220
 Val Gly Glu Asp Ile Gly Ile Glu Gly Arg Trp Glu Tyr Phe Asp Lys
 225 230 235 240
 Thr Gly Gln Leu Arg Asp Met Leu Gln Asn His Leu Leu Gln Ile Leu
 245 250 255
 Thr Phe Val Ala Met Glu Pro Pro Ala Asp Leu Ser Ala Glu Ser Ile
 260 265 270
 His Met Glu Lys Ile Lys Val Leu Lys Ala Leu Arg Pro Ile Thr Val
 275 280 285
 Arg Asn Val Glu Glu Lys Thr Val Arg Gly Gln Tyr Thr Ala Gly Phe
 290 295 300
 Ile Lys Gly Lys Ser Val Pro Gly Tyr Leu Glu Glu Gly Ala Asn
 305 310 315 320
 Thr Glu Ser Thr Thr Glu Thr Phe Val Ala Ile Arg Val Asp Ile Asp
 325 330 335
 Asn Trp Arg Trp Ala Gly Val Pro Phe Tyr Met Arg Thr Gly Lys Arg
 340 345 350
 Thr Pro Asn Lys Arg Thr Glu Ile Val Val Asn Phe Lys Gln Leu Pro
 355 360 365
 His Asn Ile Phe Lys Asp Ser Phe His Glu Leu Pro Ala Asn Lys Leu
 370 375 380
 Val Ile His Leu Gln Pro Asn Glu Gly Val Asp Val Met Met Leu Asn
 385 390 395 400
 Lys Val Pro Gly Ile Asp Gly Asn Ile Lys Leu Gln Gln Thr Lys Leu
 405 410 415
 Asp Leu Ser Phe Ser Glu Thr Phe Lys Lys Asn Arg Ile Phe Gly Gly
 420 425 430
 Tyr Glu Lys Leu Ile Leu Glu Ala Leu Arg Gly Asn Pro Thr Leu Phe
 435 440 445
 Leu Ser Arg Glu Glu Ile Glu Gln Ala Trp Thr Trp Val Asp Ser Ile
 450 455 460
 Gln Asp Ala Trp Gln His Asn His Thr Pro Pro Lys Pro Tyr Pro Ala
 465 470 475 480

Gly Ser Trp Gly Pro Val Ala Ser Val Ala Leu Leu Ala Arg Asp Gly
485 490 495

Arg Ala Trp Glu Glu
500

<210> 11
<211> 984
<212> DNA
<213> METHYLOMONAS SP.

<400> 11
atggcaagaa acttacttga gcaactccgc gagatgaccc ttgttggc cgataccgg 60
gacatccagg cgatcgaaac cttcaagccg cgcatgc aa cggccaaccc gtctttgatc 120
accggccgccc cgcaaattgcc gcaatataa ggcatcggtt acgacaccc taaaagggtgcg 180
cgtgcgacgt tgggtgccag cgcttcggct gccgagggtgg ctcatggc gttcgatcg 240
ttggcggttt ctccgggtt gaaaatcctg gaaatcatcg aaggtcggtt ttccaccggag 300
gttgatgcgc gtttgtcta tgacaccgaa ggcactattt ccaaaaggccg ggatctgatc 360
aaacaatacg aagctgcagg tggttccaaa gagcgcgtac tgatcaaat tgccgcgacc 420
tgggaaggca tccaggccgc tgccgtttt gaaaaagaag gtattcacac caacttgacc 480
ctgttggtcg gtctgcacca ggcgattgtt gttggcggaaa acggcattac cctgatttct 540
ccgtttgtcg gccgtattct ggactgggtac aaaaaagaca ctggccgcga ctcttatcct 600
tccaacgaag atcttgcgtt attgtctgtt actgaagttt ataactacta caaaaaattt 660
ggttataaaa ctgaagtcat gggcgcgagc ttccgttaaca tcggcgaaat caccgaattt 720
gcgggttgcg atctgttgac catcgcgcct tctctgtt ccgaactgca atccgttggaa 780
ggtgatttgc cacgcaact ggaccctgca aaagcagccg gttcttcgtt cgaaaaaatc 840
agcgttgaca aagcgacttt cgagcgcgtt cacgaagaaa accgcgttgc caaagaaaaa 900
ctggccgaag gtatcgacgg ttttgcggaaa gcgttggaaa ctttgaaaaa attgttggcg 960
gatcggttgg ctgctctgga agca 984

<210> 12
<211> 328
<212> PRT
<213> METHYLOMONAS SP.

<400> 12
Met ala Arg Asn Leu Leu Glu Gln Leu Arg Glu Met Thr Val Val Val
1 5 10 15

Ala Asp Thr Gly Asp Ile Gln Ala Ile Glu Thr Phe Lys Pro Arg Asp
20 25 30

Ala Thr Thr Asn Pro Ser Leu Ile Thr Ala Ala Gln Met Pro Gln
35 40 45

Tyr Gln Gly Ile Val Asp Asp Thr Leu Lys Gly Ala Arg Ala Thr Leu
50 55 60

Gly Ala Ser Ala Ser Ala Ala Glu Val Ala Ser Leu Ala Phe Asp Arg
65 70 75 80

Leu Ala Val Ser Phe Gly Leu Lys Ile Leu Glu Ile Ile Glu Gly Arg
85 90 95

Val Ser Thr Glu Val Asp Ala Arg Leu Ser Tyr Asp Thr Glu Gly Thr
100 105 110

Ile Ala Lys Gly Arg Asp Leu Ile Lys Gln Tyr Glu Ala Ala Gly Val
 115 120 125
 Ser Lys Glu Arg Val Leu Ile Lys Ile Ala Ala Thr Trp Glu Gly Ile
 130 135 140
 Gln Ala Ala Ala Val Leu Glu Lys Glu Gly Ile His Thr Asn Leu Thr
 145 150 155 160
 Leu Leu Phe Gly Leu His Gln Ala Ile Ala Cys Ala Glu Asn Gly Ile
 165 170 175
 Thr Leu Ile Ser Pro Phe Val Gly Arg Ile Leu Asp Trp Tyr Lys Lys
 180 185 190
 Asp Thr Gly Arg Asp Ser Tyr Pro Ser Asn Glu Asp Pro Gly Val Leu
 195 200 205
 Ser Val Thr Glu Val Tyr Asn Tyr Tyr Lys Lys Phe Gly Tyr Lys Thr
 210 215 220
 Glu Val Met Gly Ala Ser Phe Arg Asn Ile Gly Glu Ile Thr Glu Leu
 225 230 235 240
 Ala Gly Cys Asp Leu Leu Thr Ile Ala Pro Ser Leu Leu Ala Glu Leu
 245 250 255
 Gln Ser Val Glu Gly Asp Leu Pro Arg Lys Leu Asp Pro Ala Lys Ala
 260 265 270
 Ala Gly Ser Ser Ile Glu Lys Ile Ser Val Asp Lys Ala Thr Phe Glu
 275 280 285
 Arg Met His Glu Glu Asn Arg Met ala Lys Glu Lys Leu Ala Glu Gly
 290 295 300
 Ile Asp Gly Phe Ala Lys Ala Leu Glu Thr Leu Glu Lys Leu Leu Ala
 305 310 315 320
 Asp Arg Leu Ala Ala Leu Glu Ala
 325

<210> 13
 <211> 480
 <212> DNA
 <213> METHYLOMONAS SP.

<400> 13
 atggccgcgg gccccgtggg cttgacgcaa ttgctgccag aactggccga agctatttgt 60
 ccgacgagcc gattcatgt gcaggtcatt ggtgacacgg tggaggacat cgttgcggaa 120
 gccaaacggc tacacgattt gcccgtcgac atagtggtga aaattccggc gcatggcgcc 180
 ggactggccgg ccatcaagca gatcaagcgc cacgatattc cggtgctggc gacagcgatt 240
 tacaacgtgc agcaagggtt gctggccgt ttgaacggcg ccgattatct ggccgccttat 300
 ctgaatcgcg tcgataacca gggtttgac ggtattggcg tggtcgcccga tctgcagagc 360
 ttgatcgacc ggtatcaaat gcccacccaa ctcctggtag cgagcttcaa aaacgtacaa 420
 caggtgctgc aggtgttcaa actggccgtg gcgtcggtga cgctgcctt ggacatttg 480

<210> 14
<211> 160
<212> PRT
<213> METHYLOMONAS SP.

<400> 14
Met ala Ala Gly Gly Val Gly Leu Thr Gln Leu Leu Pro Glu Leu Ala
1 5 10 15

Glu Ala Ile Gly Pro Thr Ser Arg Phe His Val Gln Val Ile Gly Asp
20 25 30

Thr Val Glu Asp Ile Val Ala Glu Ala Lys Arg Leu His Asp Leu Pro
35 40 45

Val Asp Ile Val Val Lys Ile Pro Ala His Gly Ala Gly Leu Ala Ala
50 55 60

Ile Lys Gln Ile Lys Arg His Asp Ile Pro Val Leu Ala Thr Ala Ile
65 70 75 80

Tyr Asn Val Gln Gln Gly Trp Leu Ala Ala Leu Asn Gly Ala Asp Tyr
85 90 95

Leu Ala Pro Tyr Leu Asn Arg Val Asp Asn Gln Gly Phe Asp Gly Ile
100 105 110

Gly Val Val Ala Asp Leu Gln Ser Leu Ile Asp Arg Tyr Gln Met Pro
115 120 125

Thr Lys Leu Leu Val Ala Ser Phe Lys Asn Val Gln Gln Val Leu Gln
130 135 140

Val Leu Lys Leu Gly Val Ala Ser Val Thr Leu Pro Leu Asp Ile Val
145 150 155 160

<210> 15
<211> 1005
<212> DNA
<213> METHYLOMONAS SP.

<400> 15
atggcttag tgcattgcg acaactttt gattatgcgg ccgagcatgg ctttgcgtg 60
ccggcggtca acgtcagcaa catggagcg gtacaggcca tcatacgaggc ggccgctgcc 120
tgcgatagtc cagtgatcat gcaaggttcg gcccggcaca accgctatgc cggcgaagtg 180
tttctacggc atttgatatt ggcggccgtg gagcaatatac cgcatattcc ggtcgatcg 240
caccgcgacc atgcacccac gcccgcacatc tgccgcgaag ccataacaatc gggcttcagc 300
tcggtgatga tggacggttc gttgctggca gacataaaaa ccccggttc tttgcatac 360
aacgtcgacg tcacccgcac cgtggtcaag atggcgcatg cctgcggcgt atcggtggaa 420
ggcgaaatcg gtcgcctggg agcgctggag gccaagtccg cgcaagatca cagccgtttg 480
ctgaccgatc ccgacgaaagc ggtcgaattc gtcgaacaga cccaggtcga tgccgtggcc 540
gtggccatcg gcaccagcca cggcgcttat aaattcagca agccgcccac cggcgaagtg 600
ctggtgatca gtcgattgaa agaactgcag caacgactgc caaataccca ttttgtatg 660
catggctcca gttcggtgcc gcaggattgg ttgaaaatca tcaacgatta tggcggcgat 720
attccggaaa cctatggcgt gccggcgtaa gaaatcgtcg aaggcataaa atatggtg 780
cgcaaggatca acatcgatac cgacctgcgc atggcgtcca ccggcgcgat gcgcagggtt 840

ctggcccaac cgaaaaacgc ctcggagcta gacgcgcgca agacctatca agccgccagg 900
gacgcaatgc aggattatg ccaggctcgc tacgaagcgt tcgggtcggc gggacatgcc 960
ggcaaaatca aaccggtttc actggccggca atggccaaac gctat 1005

<210> 16
<211> 335
<212> PRT
<213> METHYLOMONAS SP.

<400> 16
Met ala Leu Val Ser Leu Arg Gln Leu Leu Asp Tyr Ala Ala Glu His
1 5 10 15

Gly Phe Ala Val Pro Ala Phe Asn Val Ser Asn Met Glu Gln Val Gln
20 25 30

Ala Ile Met Gln Ala Ala Ala Cys Asp Ser Pro Val Ile Met Gln
35 40 45

Gly Ser Ala Gly Ala Asn Arg Tyr Ala Gly Glu Val Phe Leu Arg His
50 55 60

Leu Ile Leu Ala Ala Val Glu Gln Tyr Pro His Ile Pro Val Val Met
65 70 75 80

His Arg Asp His Ala Pro Thr Pro Asp Ile Cys Ala Gln Ala Ile Gln
85 90 95

Ser Gly Phe Ser Ser Val Met Met Asp Gly Ser Leu Leu Ala Asp Met
100 105 110

Lys Thr Pro Ala Ser Phe Ala Tyr Asn Val Asp Val Thr Arg Thr Val
115 120 125

Val Lys Met ala His Ala Cys Gly Val Ser Val Glu Gly Glu Ile Gly
130 135 140

Cys Leu Gly Ala Leu Glu Ala Lys Ser Ala Gln Asp His Ser Arg Leu
145 150 155 160

Leu Thr Asp Pro Asp Glu Ala Val Glu Phe Val Glu Gln Thr Gln Val
165 170 175

Asp Ala Val Ala Val Ala Ile Gly Thr Ser His Gly Ala Tyr Lys Phe
180 185 190

Ser Lys Pro Pro Thr Gly Glu Val Leu Val Ile Ser Arg Leu Lys Glu
195 200 205

Leu Gln Gln Arg Leu Pro Asn Thr His Phe Val Met His Gly Ser Ser
210 215 220

Ser Val Pro Gln Asp Trp Leu Lys Ile Ile Asn Asp Tyr Gly Gly Asp
225 230 235 240

Ile Pro Glu Thr Tyr Gly Val Pro Val Glu Glu Ile Val Glu Gly Ile
245 250 255

Lys	Tyr	Gly	Val	Arg	Lys	Val	Asn	Ile	Asp	Thr	Asp	Leu	Arg	Met	ala
			260				265					270			
Ser	Thr	Gly	Ala	Met	Arg	Arg	Phe	Leu	Ala	Gln	Pro	Glu	Asn	Ala	Ser
	275				280					285					
Glu	Leu	Asp	Ala	Arg	Lys	Thr	Tyr	Gln	Ala	Ala	Arg	Asp	Ala	Met	Gln
	290				295				300						
Ala	Leu	Cys	Gln	Ala	Arg	Tyr	Glu	Ala	Phe	Gly	Ser	Ala	Gly	His	Ala
305				310				315				320			
Gly	Lys	Ile	Lys	Pro	Val	Ser	Leu	Ala	Ala	Met	ala	Lys	Arg	Tyr	
				325				330				335			

<210> 17
<211> 1074
<212> DNA
<213> METHYLOMONAS SP.

<400> 17

atgacaaaaaa	tcttagatgt	tgtaaaaacc	ggcggtgtca	ccggtaaga	tgtgc	aaaaaa	60
attttcgcaa	tctgcaaaga	aaacaactt	gccttgccag	ccgtcaacgt	gatcagtacc		120
gataccatta	atgcggatt	ggaagcggcc	gccaaaggcca	aatcacctgt	tgttatccag		180
ttttcaaatg	gcggcgcggc	tttcgttgcc	ggtaaagggtt	tgaaaattgga	aggtaaggc		240
tgttcgattc	atggtgccat	ttcaggtgct	caccacgttc	accgcttggc	ggaactctat		300
ggtgtacctg	tcgttctgca	taccgaccac	gcggcgaaaa	aattgctgcc	atgggtagat		360
ggtatgctgg	atgaagggtga	aaaattctt	gcggccaccg	gcaaggctt	gttcagctcg		420
cacatgctgg	acttgtccga	agagagcctg	gaagaaaaaca	tgc	aaatctg	cggtaaatac	480
ttggcgcgca	tggcgaaaaat	gggtatgacc	ttggaaatcg	aactgggctg	caccggcggt		540
gaagaagacg	gcgtggacaa	cagcggcatg	gatcattccg	cgttgtacac	ccagccgaa		600
gacgtggctt	acgcgtatga	gcacctgagc	aaaatcagcc	ctaacttcac	gattgcgct		660
tctttcgcga	acgtgcacgg	cgttactcg	ccaggaaacg	tcaagctgac	gcca	aaaaatt	720
ctggataact	cgcaaaaaata	cgtatccgaa	aaattcggct	tgccagctaa	atcattgacc		780
ttcgtattcc	atggcggctc	tgg	ttcgtct	ccggaaagaaa	tcaaggaatc	catcagctat	840
ggcgtatgt	aaatgaacat	cgataccgat	acccaatggg	caac	ctgggaa	aggcgtatg	900
aacttctaca	agaaaaaacga	aggctatctg	caaggccaga	tgc	ggcaatcc	ggaagggtgcc	960
gacaagccga	acaaaaaaaata	ctatgaccca	cgcgtatggc	aac	gtgccgg	ccaagaaggc	1020
atggttgcac	gtctgcaaca	agcattccag	gaattgaatg	cag	taaacac	gctg	1074

<210> 18
<211> 358
<212> PRT
<213> METHYLOMONAS SP.

<400> 18

Met	Thr	Lys	Ile	Leu	Asp	Val	Val	Lys	Pro	Gly	Val	Val	Thr	Gly	Glu
1				5				10				15			
Asp	Val	Gln	Lys	Ile	Phe	Ala	Ile	Cys	Lys	Glu	Asn	Asn	Phe	Ala	Leu
				20				25				30			
Pro	Ala	Val	Asn	Val	Ile	Ser	Thr	Asp	Thr	Ile	Asn	Ala	Val	Leu	Glu
				35				40				45			
Ala	Ala	Ala	Lys	Ala	Lys	Ser	Pro	Val	Val	Ile	Gln	Phe	Ser	Asn	Gly
				50				55				60			

Gly Ala Ala Phe Val Ala Gly Lys Gly Leu Lys Leu Glu Gly Gln Gly
 65 70 75 80
 Cys Ser Ile His Gly Ala Ile Ser Gly Ala His His Val His Arg Leu
 85 90 95
 Ala Glu Leu Tyr Gly Val Pro Val Val Leu His Thr Asp His Ala Ala
 100 105 110
 Lys Lys Leu Leu Pro Trp Val Asp Gly Met Leu Asp Glu Gly Glu Lys
 115 120 125
 Phe Phe Ala Ala Thr Gly Lys Pro Leu Phe Ser Ser His Met Leu Asp
 130 135 140
 Leu Ser Glu Glu Ser Leu Glu Glu Asn Ile Glu Ile Cys Gly Lys Tyr
 145 150 155 160
 Leu Ala Arg Met Ala Lys Met Gly Met Thr Leu Glu Ile Glu Leu Gly
 165 170 175
 Cys Thr Gly Gly Glu Glu Asp Gly Val Asp Asn Ser Gly Met Asp His
 180 185 190
 Ser Ala Leu Tyr Thr Gln Pro Glu Asp Val Ala Tyr Ala Tyr Glu His
 195 200 205
 Leu Ser Lys Ile Ser Pro Asn Phe Thr Ile Ala Ala Ser Phe Gly Asn
 210 215 220
 Val His Gly Val Tyr Ser Pro Gly Asn Val Lys Leu Thr Pro Lys Ile
 225 230 235 240
 Leu Asp Asn Ser Gln Lys Tyr Val Ser Glu Lys Phe Gly Leu Pro Ala
 245 250 255
 Lys Ser Leu Thr Phe Val Phe His Gly Gly Ser Gly Ser Ser Pro Glu
 260 265 270
 Glu Ile Lys Glu Ser Ile Ser Tyr Gly Val Val Lys Met Asn Ile Asp
 275 280 285
 Thr Asp Thr Gln Trp Ala Thr Trp Glu Gly Val Met Asn Phe Tyr Lys
 290 295 300
 Lys Asn Glu Gly Tyr Leu Gln Gly Gln Ile Gly Asn Pro Glu Gly Ala
 305 310 315 320
 Asp Lys Pro Asn Lys Lys Tyr Tyr Asp Pro Arg Val Trp Gln Arg Ala
 325 330 335
 Gly Gln Glu Gly Met Val Ala Arg Leu Gln Gln Ala Phe Gln Glu Leu
 340 345 350
 Asn Ala Val Asn Thr Leu
 355

<210> 19
 <211> 636

<212> DNA

<213> METHYLOMONAS SP.

<400> 19

gaaaatacta tgtccgtcac catcaaagaa gtcatgacca cctcgccgt tatgccggtc 60
atggtcatca atcatctgga acatgccgtc cctctggctc ggcgcgtact cgacggtgtgc 120
ttgaaagttt tggagatcac attgcgcacg ccgggtggcac tggaatgtat cgcacgtatc 180
aaagccgaag taccggacgc catcgctggc gcgggcacca tcatacacc tcataaccc 240
tatcaagcga ttgacgcccgg tgcggattc atcgctcagcc ccggcatcac cgaaaatcta 300
ctcaacgaag cgcttagcatc cggcgtgcct atcctgcccgc ggcgtcatcac acccagcgag 360
gtcatgcgtt tattggaaaa aggcatcaat ggcgtgaaat tcttccggc tgaaggcc 420
ggccgcatac cgatgctgaa atcccttggc ggcccccttgc cgcaagtac cttctgtccg 480
accggcggcg tcaatccaa aaacgcgccc gaatatctgg cattgaaaaa tgtcgcctgc 540
gtcggcggct cctggatggc gccggccgat ctggtagatg ccgaagactg ggcggaaatc 600
acgcggcggg cgagcgaggc cggcgcattt aaaaaa 636

<210> 20

<211> 212

<212> PRT

<213> METHYLOMONAS SP.

<400> 20

Glu Asn Thr Met Ser Val Thr Ile Lys Glu Val Met Thr Thr Ser Pro
1 5 10 15

Val Met Pro Val Met Val Ile Asn His Leu Glu His Ala Val Pro Leu
20 25 30

Ala Arg Ala Leu Val Asp Gly Gly Leu Lys Val Leu Glu Ile Thr Leu
35 40 45

Arg Thr Pro Val Ala Leu Glu Cys Ile Arg Arg Ile Lys Ala Glu Val
50 55 60

Pro Asp Ala Ile Val Gly Ala Gly Thr Ile Ile Asn Pro His Thr Leu
65 70 75 80

Tyr Gln Ala Ile Asp Ala Gly Ala Glu Phe Ile Val Ser Pro Gly Ile
85 90 95

Thr Glu Asn Leu Leu Asn Glu Ala Leu Ala Ser Gly Val Pro Ile Leu
100 105 110

Pro Gly Val Ile Thr Pro Ser Glu Val Met Arg Leu Leu Glu Lys Gly
115 120 125

Ile Asn Ala Met Lys Phe Phe Pro Ala Glu Ala Ala Gly Gly Ile Pro
130 135 140

Met Leu Lys Ser Leu Gly Gly Pro Leu Pro Gln Val Thr Phe Cys Pro
145 150 155 160

Thr Gly Gly Val Asn Pro Lys Asn Ala Pro Glu Tyr Leu Ala Leu Lys
165 170 175

Asn Val Ala Cys Val Gly Gly Ser Trp Met Ala Pro Ala Asp Leu Val
180 185 190

Asp Ala Glu Asp Trp Ala Glu Ile Thr Arg Arg Ala Ser Glu Ala Ala
195 200 205

Ala Leu Lys Lys
210

<210> 21
<211> 873
<212> DNA
<213> Methyloimonas 16a

<400> 21
atgaaaagttt ccaaaggcgt tttcccggtt gccggactgg gcacccggtc attgcccgc 60
accaaggccg ttgccaagga aatgttgcgg gtgggtggaca agccgctgat tcagtatgcg 120
gtggaaaggagg ccgtggccgc cgccatcgac acgatgattt tcgtgtatcg 180
aatccattt ccaaccattt cgataaaatcc tacgaactgg aaaaggaact ggaaaaaaagc 240
ggcaagaccg atttgctgaa aatgctgcgg gagattttgc cgcgcatgt gtcctgcgt 300
ttcgtgcgtc aagcggaggc tctgggtttt gggcatgcgg tgcattgcgc caagccgtg 360
gtcggcaacg agccgtttgc ggtgatcttgc ccggatgact tgatcgagga cggcgagcgc 420
ggttgcatga agcagatggt ggattttttc gacaaagagc aaagcagcgt attgggggt 480
gagcgggtcg atcccaagga aacccataag tacggcatcg tcgaacatgc cgaaacatcg 540
cccagagtgcg gttgggtttagt ttccatcggtc gagaacccca aaccgcgaaatggccccc 600
aatatcgccg tggcggccgc ctacatcttgc acgcccggcca tttttcaaaa aatcgagaac 660
acggggcgcg gcccggccgc cgaaattcaa ttgaccgatgcgattgcgc gttgatgaaa 720
gacgaacgcg tttgtccta tgaattcgaa ggcaatcgct acgactgcgg ttccaagttt 780
ggtttttgttggccaaatgt cgaatatggc ttgctgcaca aggaatcaa agccgaattc 840
gccaactatc tgaacaacaacg cgtcagcaaa atc 873

<210> 22
<211> 293
<212> PRT
<213> Methyloimonas 16a

<400> 22
Met Thr Met Lys Val Thr Lys Ala Val Phe Pro Val Ala Gly Leu Gly
1 5 10 15

Thr Arg Ser Leu Pro Ala Thr Lys Ala Val Ala Lys Glu Met Leu Pro
20 25 30

Val Val Asp Lys Pro Leu Ile Gln Tyr Ala Val Glu Glu Ala Val Ala
35 40 45

Ala Gly Ile Asp Thr Met Ile Phe Val Ile Gly Arg Asn Lys Glu Ser
50 55 60

Ile Ala Asn His Phe Asp Lys Ser Tyr Glu Leu Glu Lys Glu Leu Glu
65 70 75 80

Lys Ser Gly Lys Thr Asp Leu Leu Lys Met Leu Arg Glu Ile Leu Pro
85 90 95

Ala His Val Ser Cys Val Phe Val Arg Gln Ala Glu Ala Leu Gly Leu
100 105 110

Gly His Ala Val His Cys Ala Lys Pro Val Val Gly Asn Glu Pro Phe
115 120 125

Ala Val Ile Leu Pro Asp Asp Leu Ile Glu Asp Gly Glu Arg Gly Cys
 130 135 140

 Met Lys Gln Met Val Asp Leu Phe Asp Lys Glu Gln Ser Ser Val Leu
 145 150 155 160

 Gly Val Glu Arg Val Asp Pro Lys Glu Thr His Lys Tyr Gly Ile Val
 165 170 175

 Glu His Ala Glu Thr Ser Pro Arg Val Gly Trp Leu Ser Ser Ile Val
 180 185 190

 Glu Lys Pro Lys Pro Glu Val Ala Pro Ser Asn Ile Ala Val Val Gly
 195 200 205

 Arg Tyr Ile Leu Thr Pro Ala Ile Phe Gln Lys Ile Glu Asn Thr Gly
 210 215 220

 Arg Gly Ala Gly Gly Glu Ile Gln Leu Thr Asp Ala Ile Ala Ala Leu
 225 230 235 240

 Met Lys Asp Glu Arg Val Leu Ser Tyr Glu Phe Glu Gly Asn Arg Tyr
 245 250 255

 Asp Cys Gly Ser Lys Phe Gly Phe Leu Leu Ala Asn Val Glu Tyr Gly
 260 265 270

 Leu Leu His Lys Glu Ile Lys Ala Glu Phe Ala Asn Tyr Leu Lys Gln
 275 280 285

 Arg Val Ser Lys Ile
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<210> 23
 <211> 1419
 <212> DNA
 <213> Methyloimonas 16a

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 atcttgggtg cgatcatatt tttcgagatc ggccaggtgt atcggccgtg gcgcaatgac 240
 gcgatgcgcg gcgaaattcc ccgcattcattc agagcctgtt tgctggcattt gctgacggtg 300
 gtgtccatcg tggcccttgtt cagatttgcatttttttttgg gttccagttt tcgctggatc 360
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 gtgttgaagt ggttgcgtgc acggggctgg agccaggggc gcatattttt ggtgggtttt 480
 aatcagatgg ccgtcgccgt cagtcggcaa ttgaatactt cttctggc cgggttgcag 540
 gtgattgtt atgtcgatga cggggccgaa gaccggctgg cgggtggcgaa ttattcgctg 600
 ccacgcctgg gcaagtttgcag cgatctgcct cgtctggttt ccagacaagc cgtggatgaa 660
 gtctgggtgg cgtttccctgg cgcttcgcgt gcccggc tacagcacaatttgcatt 720
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 atcagcccgat tgatgcgtt cattgcgtt ggcgtgaaac tgaggatctcc gggccgggtg 960
 ttttacaagc aggtcagatgg gggctggaaac aatcgcaaat tcacgatgtt gaagtttcgt 1020
 tcgatgcggc tcatgcggc ggcggaaacc ggcggcgtt gggccaggcc cggcgaaaac 1080
 cgtgcaaccc ggtttggggc ttccctgcgc aaaaccagtc tggacgagtt gccgcagttg 1140
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gtcgaggtgt tcaaggatca agtacccaat tacatgaaaa aacacatggc caaggcgggc 1260
 attaccgtt gggcacaagt caacggctgg cgcggtgata ccgacctgaa tcgcccac 1320
 gaacacgatc tgtattacat ccagcattgg tcggtctggc tcgatctgga gattgccttt 1380
 cgcaccgtgt tgaccggctt tatcaacaaa aatgcctat 1419

<210> 24

<211> 473

<212> PRT

<213> Methyloimonas 16a

<400> 24

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Gly	His	Thr	Val	Ile	Leu	Leu	Leu	Arg	Val	Ile	Asp	Val	Val	Met	Leu
			20					25							30

Leu	Gly	Ala	Ala	Trp	Leu	Ala	His	Tyr	Phe	Trp	Leu	His	Asp	Ser	Val
			35				40				45				

Ile	Asp	Gln	His	Tyr	Arg	Phe	Val	Ile	Ala	Leu	Gly	Ile	Leu	Gly	Ala
			50			55				60					

Ile	Ile	Phe	Phe	Glu	Ile	Gly	Gln	Val	Tyr	Arg	Pro	Trp	Arg	Asn	Asp
			65			70			75			80			

Ala	Met	Arg	Gly	Glu	Ile	Pro	Arg	Ile	Ile	Arg	Ala	Trp	Leu	Leu	Ala
			85				90				95				

Leu	Leu	Thr	Val	Val	Ser	Ile	Val	Ala	Leu	Val	Arg	Leu	His	Phe	Trp
			100				105				110				

Phe	Gly	Ser	Ser	Tyr	Arg	Trp	Ile	Ala	Ser	Trp	Gly	Gly	Leu	Gly	Leu
			115			120				125					

Phe	Phe	Val	Leu	Ala	Ala	Arg	Gly	Val	Leu	Ala	Gln	Val	Leu	Lys	Trp
			130			135				140					

Leu	Arg	Ala	Arg	Gly	Trp	Ser	Gln	Gly	Arg	Ile	Ile	Leu	Val	Gly	Leu
			145			150			155			160			

Asn	Gln	Met	ala	Val	Ala	Val	Ser	Arg	Gln	Leu	Asn	His	Ser	Ser	Trp
			165				170				175				

Ala	Gly	Leu	Gln	Val	Ile	Gly	Tyr	Val	Asp	Asp	Arg	Ala	Glu	Asp	Arg
			180			185				190					

Leu	Ala	Val	Ala	Asp	Tyr	Ser	Leu	Pro	Arg	Leu	Gly	Lys	Leu	Ser	Asp
			195			200				205					

Leu	Pro	Arg	Leu	Val	Ser	Arg	Gln	Ala	Val	Asp	Glu	Val	Trp	Val	Ala
			210			215				220					

Phe	Pro	Gly	Ala	Ser	Leu	Ala	Glu	Arg	Val	Gln	His	Glu	Leu	Arg	His
			225			230			235			240			

Leu	Pro	Val	Ser	Ile	Arg	Leu	Val	Ile	Asp	Cys	Phe	Ala	Phe	Lys	Gln
			245			250			255			255			

Ser Lys Phe Leu Ser Leu Asn Thr Val Ala Gly Ile Pro Thr Leu Asp
 260 265 270
 Val Ser Val Ser Pro Leu His Gly Val Asn Arg Tyr Ile Lys Glu Ile
 275 280 285
 Glu Asp Arg Leu Leu Ala Leu Leu Leu Leu Ile Ser Pro Leu
 290 295 300
 Met Leu Val Ile Ala Leu Gly Val Lys Leu Ser Ser Pro Gly Pro Val
 305 310 315 320
 Phe Tyr Lys Gln Val Arg Val Gly Trp Asn Asn Arg Lys Phe Thr Met
 325 330 335
 Leu Lys Phe Arg Ser Met Pro Val Asp Ala Glu Ala Lys Thr Gly Ala
 340 345 350
 Val Trp Ala Arg Pro Gly Glu Asn Arg Ala Thr Arg Phe Gly Ala Phe
 355 360 365
 Leu Arg Lys Thr Ser Leu Asp Glu Leu Pro Gln Leu Ile Asn Val Leu
 370 375 380
 Lys Gly Asp Met Ser Leu Val Gly Pro Arg Pro Glu Arg Pro Asp Phe
 385 390 395 400
 Val Glu Val Phe Lys Asp Gln Val Pro Asn Tyr Met Lys Lys His Met
 405 410 415
 Val Lys Ala Gly Ile Thr Gly Trp Ala Gln Val Asn Gly Trp Arg Gly
 420 425 430
 Asp Thr Asp Leu Asn Arg Arg Ile Glu His Asp Leu Tyr Tyr Ile Gln
 435 440 445
 His Trp Ser Val Trp Phe Asp Leu Glu Ile Ala Phe Arg Thr Val Leu
 450 455 460
 Thr Gly Phe Ile Asn Lys Asn Ala Tyr
 465 470

<210> 25
 <211> 1098
 <212> DNA
 <213> Methyloimonas 16a

<400> 25
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 gggcagtgg tcaaggagaa aacccgcatt cagccgatca cccggattt gatcatcgag 180
 cgtgaagtgc cacggcggca agccgtcaac aatctaccgc cgatggacga aacccggacc 240
 agttatcgca tcgtccgca ggacaggtt caaatcacgg tatggagca tcccgaaactg 300
 aacgatccc gcgccgagaa aatcctgccg gaactggccg gcaaggtcgt ggacgataac 360
 ggcgatttgt attaccccta tgtcggtacc cttcatgtcg gcggcaagac cgtcaccgaa 420
 gtgcgcgagg aattgacccg cgaactgtcc aaataacttca aaaaggtcaa actcgacatt 480
 cgtgtgtgt cgttccaggc tcaccgggtc ggggtggtcg gtgaagtcag aaatccccgc 540
 atcgtcgcga tgaccgaaac gccgttgacg gtggcagaag ccatcagcag ggccggccgc 600
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<210> 26

<211> 366

<212> PRT

<213> Methylomonas 16a

<400> 26

Met	Phe	Arg	Leu	Ile	Pro	Ile	Met	Leu	Val	Leu	Leu	Leu	Pro	Gly	Cys
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Phe	Leu	Ala	Pro	Gly	Met	Asp	Met	Gln	Thr	Asp	Gly	Asp	Leu	Thr	Glu
													20	25	30

Ile	Glu	Leu	Pro	Thr	Met	Lys	Gly	Gly	Gln	Leu	Val	Lys	Glu	Lys	Thr
													35	40	45

Arg	Ile	Gln	Pro	Ile	Thr	Ala	Asp	Leu	Ile	Glu	Arg	Glu	Val	Ala	
													50	55	60

Arg	Arg	Gln	Ala	Val	Asn	Asn	Leu	Pro	Pro	Met	Asp	Glu	Thr	Arg	Thr	
													65	70	75	80

Ser	Tyr	Arg	Ile	Gly	Pro	Gln	Asp	Arg	Leu	Gln	Ile	Thr	Val	Trp	Glu
													85	90	95

His	Pro	Glu	Leu	Asn	Asp	Pro	Gly	Gly	Glu	Lys	Ile	Leu	Pro	Glu	Leu
													100	105	110

Ala	Gly	Lys	Val	Val	Asp	Asp	Asn	Gly	Asp	Leu	Tyr	Tyr	Pro	Tyr	Val
													115	120	125

Gly	Thr	Leu	His	Val	Gly	Gly	Lys	Thr	Val	Thr	Glu	Val	Arg	Glu	Glu
													130	135	140

Leu	Thr	Arg	Glu	Leu	Ser	Lys	Tyr	Phe	Lys	Lys	Val	Lys	Leu	Asp	Ile	
													145	150	155	160

Arg	Val	Leu	Ser	Phe	Gln	Ala	His	Arg	Val	Ala	Val	Val	Gly	Glu	Val
													165	170	175

Arg	Asn	Pro	Gly	Ile	Val	Ala	Met	Thr	Glu	Thr	Pro	Leu	Thr	Val	Ala
													180	185	190

Glu	Ala	Ile	Ser	Arg	Ala	Gly	Gly	Ala	Thr	Gln	Asp	Ser	Asp	Leu	Asn
													195	200	205

Asn	Val	Ala	Leu	Ala	Arg	Gly	Gly	Arg	Leu	Tyr	Lys	Leu	Asp	Val	Gln
													210	215	220

Ala	Leu	Tyr	Glu	Lys	Gly	Leu	Thr	Thr	Gln	Asn	Leu	Leu	Leu	Arg	Asp	
													225	230	235	240

Gly Asp Val Leu Asn Val Gly Asp Gln Lys Asp Ser Lys Val Tyr Val
 245 250 255
 Met Gly Glu Val Gly Arg Gln Gln Ala Ile Gln Ile Asn Lys Gly Arg
 260 265 270
 Met Ser Leu Ala Gln Ala Leu Ala Glu Ala Tyr Gly Val Asp Phe Asn
 275 280 285
 Thr Ser Arg Pro Gly Asp Ile Tyr Val Leu Arg Ala Gly Asp Met Gln
 290 295 300
 Pro Glu Ile Phe Gln Leu Asp Ala Glu Ser Pro Asp Ala Met Ile Leu
 305 310 315 320
 Ala Glu Gln Phe Pro Leu Gln Pro His Asp Thr Leu Phe Val Gly Thr
 325 330 335
 Ala Gly Val Thr Gln Trp Ser Arg Val Leu Asn Gln Ile Leu Pro Gly
 340 345 350
 Ser Phe Thr Ala Ile Met Ser Gln Ala Ala Met Met Gly Met
 355 360 365

<210> 27
 <211> 2337
 <212> DNA
 <213> Methyloimonas 16a

<400> 27
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 gacaaaaata aagccttgtt ggcggccaaat ttgcgttagcg aggcaatgg tacgccaacg 240
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 ggcaagggtgg tggaggattt gaatcttagtc gtggaggcggt cgccacgata ctttccatc 360
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<210> 28

<211> 779

<212> PRT

<213> Methylomonas 16a

<400> 28

Met	Pro	Pro	Leu	Asn	Pro	Val	Met	Met	Gln	Glu	Pro	Gly	Val	Ser	Ile
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Arg	Asp	Tyr	Val	Asp	Leu	Leu	Ile	Glu	Gly	Lys	Lys	Thr	Ile	Leu	Leu
															30
20								25							

Thr	Leu	Ala	Ile	Val	Leu	Ser	Val	Thr	Met	Ile	Tyr	Leu	Val	Leu	Ala
35								40					45		

Pro	Arg	Thr	Tyr	Lys	Ala	Asp	Ala	Leu	Leu	Arg	Ile	Asp	Lys	Asn	Lys
50						55				60					

Ala	Leu	Leu	Ala	Ala	Asn	Leu	Arg	Ser	Glu	Gly	Asn	Gly	Thr	Pro	Thr
65						70			75				80		

Glu	Ala	Glu	Asn	Pro	Arg	Ala	Gln	Arg	Glu	Val	Glu	Ile	Leu	Arg	Ser
85								90				95			

Arg	Ser	Val	Leu	Gly	Lys	Val	Val	Glu	Asp	Leu	Asn	Leu	Val	Val	Glu
100								105				110			

Ala	Ser	Pro	Arg	Tyr	Phe	Pro	Ile	Ile	Gly	Glu	Thr	Leu	Ala	Arg	Lys
115								120			125				

His	Asp	Lys	His	Glu	Gly	Val	Ala	Gly	Ala	Trp	Trp	Gly	Phe	Ser	Arg
130						135				140					

Trp	Ala	Trp	Gly	Gly	Glu	Lys	Leu	Lys	Ile	Glu	Arg	Phe	Glu	Val	Pro
145					150				155			160			

Asp	Arg	Tyr	Leu	Asp	Lys	Ala	Phe	Thr	Leu	Val	Ala	Leu	Glu	Ala	Gly
165								170			175				

Arg	Phe	Gln	Leu	Leu	Ser	Pro	Lys	Gly	Glu	Val	Leu	Ala	Glu	Gly	Leu
180								185			190				

Leu	Gly	Glu	Thr	Leu	Thr	Ala	Asp	Ile	Gly	Glu	Ala	Ser	Pro	Val	Val
195								200			205				

Val	Asn	Val	Ala	Asp	Leu	Gln	Ala	His	Tyr	Gly	Thr	Glu	Phe	Glu	Leu
210								215			220				

Arg Arg Lys Thr Ser Leu Ala Ala Ile Glu Thr Leu Gln Lys Ala Phe
 225 230 235 240
 Ser Val Lys Glu Val Ser Lys Asp Thr Asn Ile Leu Ser Val Glu Leu
 245 250 255
 Lys Gly Arg Asp Pro Glu Gln Leu Ala Lys Ser Val Asn Asp Ile Ala
 260 265 270
 Ser Ile Tyr Val Asn Ala Thr Val Asn Trp Glu Ser Ala Glu Ala Ser
 275 280 285
 Gln Lys Leu Asn Phe Leu Glu Ser Gln Leu Pro Leu Val Lys Glu Asn
 290 295 300
 Leu Glu Lys Ala Glu Gln Ala Leu Ser Ala Tyr Arg Gln Gln His Gly
 305 310 315 320
 Ala Val Asp Ile Ser Ala Glu Ala Glu Ile Leu Leu Lys Gln Ala Ser
 325 330 335
 Glu Met Glu Thr Leu Ser Ile Gln Leu Lys Gln Lys Tyr Asp Glu Gln
 340 345 350
 Ser Gln Arg Leu Glu Ser Glu His Pro Asp Met Ile Ala Thr Asn Ala
 355 360 365
 Gln Ile Arg Arg Val Ser Asn Lys Leu Ala Ala Leu Glu Lys Arg Ile
 370 375 380
 Lys Asp Leu Pro Lys Thr Gln Gln Asn Met Val Ser Leu Ser Arg Asp
 385 390 395 400
 Val Gln Val Asn Thr Glu Leu Tyr Thr Ser Leu Leu Asn Ser Ala Gln
 405 410 415
 Glu Gln Arg Ile Ala Ala Gly Ser Leu Gly Asn Ser Arg Ile Val
 420 425 430
 Asp Phe Ala Val Val Pro Glu Lys Pro Tyr Trp Pro Lys Pro Gly Leu
 435 440 445
 Leu Leu Ala Ile Ala Gly Leu Leu Gly Ile Ser Leu Gly Ser Ala Leu
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 Ile Phe Leu Arg His Ser Leu Gln Arg His Asp Asn Tyr Pro Ala Leu
 465 470 475 480
 Leu Glu Tyr Gln Val Gly Leu Pro Leu Phe Ala Ala Ile Pro His Ser
 485 490 495
 Lys Lys Gln Arg Arg Leu Ala Arg Leu Leu Asp Gln Gly Lys Glu Arg
 500 505 510
 Asp Thr Ala Ile Leu Val Ser His Asp Pro Leu Asp Ile Ser Val Glu
 515 520 525
 Ser Leu Arg Gly Leu Arg Thr Thr Leu Glu Ala Thr Leu Ala Ser Asp
 530 535 540

Glu Ser Lys Val Ile Met Val Ser Ser Pro Ala Pro Gly Met Gly Lys
 545 550 555 560
 Ser Phe Ile Ser Thr Asn Leu Ala Ala Leu Leu Ala Ser Ile Arg Lys
 565 570 575
 Arg Val Leu Ile Ile Asp Ala Asp Met Arg Asn Gly Arg Leu His Glu
 580 585 590
 Thr Phe Ala Ile Ala Lys Gln Pro Gly Leu Ser Asp Leu Leu Ser Gly
 595 600 605
 Lys Val Ser Leu Gly Asp Val Ile Val Ser Leu Pro Glu Ile Gly Val
 610 615 620
 Asp Leu Ile Pro Arg Gly Glu Met Val Leu Asn Pro Ala Glu Leu Leu
 625 630 635 640
 Val Leu Gly Asp Leu Ala Asp Thr Leu Glu Gln Leu Lys Ser Phe Tyr
 645 650 655
 Asn His Ile Val Ile Asp Ser Pro Pro Ile Leu Gly Ala Thr Asp Ala
 660 665 670
 Ala Ile Met Gly Lys His Cys Asp Ala Thr Phe Leu Val Val Lys Glu
 675 680 685
 Gly Arg Tyr Thr Ala Gln Glu Leu Glu Val Ser Phe Arg Arg Leu Gln
 690 695 700
 Gln Val Gly Val Lys Pro Asn Gly Phe Ile Ile Asn Asp Met Lys Glu
 705 710 715 720
 Gly Ser Ser Tyr Tyr Pro Tyr Tyr Gly Tyr Ala Tyr Gln Arg Asp Asp
 725 730 735
 Met Arg Gln Lys Gln Thr Thr Ala Trp Gln Ala Arg Phe Gln Asn Leu
 740 745 750
 Asn Asp Trp Met Gly Arg Gln Asp Ala Glu Tyr Leu Pro Val Ala Asp
 755 760 765
 Asp Ala Glu Glu Leu His Asp Ser Ile Arg Ala
 770 775

<210> 29
 <211> 1416
 <212> DNA
 <213> Methyloimonas 16a

<400> 29
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 ctgctggcgcg ggcgcgtgtt gtcgttagtg aaatccggctt gttcgtgttg 420

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gcccgggca	cggccttgc	tgccctggc	accgtatgt	cccagccgct	gctggcgaga	1140
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<210> 30

<211> 472

<212> PRT

<213> Methylomonas 16a

<400> 30

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Met	Leu	Asp	Trp	Leu	Arg	Gln	Lys	Asn	Leu	Leu	Gly	Asp	Ala	Cys	Trp
		20							25					30	

Ala	Leu	Ala	Gly	Gln	Leu	Leu	Ser	Ala	Leu	Ala	Leu	Ala	Gly	Thr	
									35				40	45	

Arg	Ile	Leu	Thr	Glu	Leu	Val	Thr	Pro	Ala	Val	Phe	Gly	His	Val	Ala
								50			55		60		

Leu	Leu	Asn	Gly	Phe	Val	Ala	Leu	Gly	Val	Ala	Val	Phe	Ala	Tyr	Pro
								65			70		75	80	

Phe	Ile	Cys	Ala	Gly	Met	Arg	Phe	Thr	Asn	Glu	Cys	Arg	Asn	Phe	Arg
								85			90		95		

Glu	Arg	Ala	Ala	Leu	His	Gly	Leu	Val	Phe	Ala	Leu	Thr	Thr	Arg	Ser
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Thr	Ala	Leu	Ala	Ile	Thr	Leu	Leu	Leu	Gly	Gly	Ala	Leu	Tyr	Cys	
								115			120		125		

Tyr	Phe	Val	Gly	Ser	Glu	Ile	Gly	Leu	Phe	Val	Leu	Thr	Gly	Leu	Leu
								130			135		140		

Leu	Ala	Val	Thr	Val	Arg	Arg	Glu	Leu	Gly	Ile	Gln	Leu	Met	Ile	Gly
								145			150		155		160

Glu	Arg	Lys	Gln	Arg	Gly	Ala	Ala	Leu	Trp	Gln	Thr	Ser	Asp	Ser	Ile
								165			170		175		

Leu	Arg	Pro	Val	Met	ala	Ile	Trp	Leu	Val	Trp	Gly	Leu	Gly	Gln	Ser
								180			185		190		

Pro Glu Ala Val Leu Leu Gly Tyr Val Cys Ala Ser Val Leu Ala Asn
 195 200 205

 Thr Leu Trp Thr Ile Val Ser Asp Ala Trp Gln Lys Lys Pro Thr Gly
 210 215 220

 Asp Arg Gly Phe Leu Gly Arg Gln Phe Glu Arg Gly Leu Trp Ala Tyr
 225 230 235 240

 Ala Leu Pro Leu Ile Pro Met Glu Leu Met Phe Trp Leu Asn Gly Leu
 245 250 255

 Gly Asp Arg Tyr Val Ile Gly Tyr Phe Leu Thr Ala Ala Glu Val Gly
 260 265 270

 Val Tyr Ala Ala Ala Tyr Thr Leu Val Asn Glu Ala Phe Asn Arg Ser
 275 280 285

 Ala Met Val Leu Leu Arg Thr Phe Gln Pro Ala Tyr Phe Gln Ala Val
 290 295 300

 Ser Gln Gly Lys Ser Lys Asp Ala Cys Ser Leu Leu Trp Leu Trp Ile
 305 310 315 320

 Gly Ala Val Val Val Met Ser Val Leu Gly Val Thr Leu Val Trp Leu
 325 330 335

 Cys Lys Asp Trp Leu Val Ala Gly Leu Leu Ala Glu Pro Tyr His Ala
 340 345 350

 Ala Gly Ala Leu Met Pro Val Ile Ala Ala Gly Thr Ala Leu His Ala
 355 360 365

 Leu Gly Thr Val Met Ser Gln Pro Leu Leu Ala Arg Lys Arg Thr Pro
 370 375 380

 Ile Leu Leu Arg Gly Arg Ile Cys Gly Ala Leu Ala Ala Leu Ile Thr
 385 390 395 400

 Leu Pro Leu Leu Val Ala His Phe Gly Leu Phe Gly Ala Ala Leu Ala
 405 410 415

 Asn Pro Val Tyr Phe Gly Ile Glu Ala Leu Val Leu Ala Leu Leu Ala
 420 425 430

 Lys Pro Trp Arg Lys Leu Arg Thr Gly Arg Gln Ala Arg Ile Val Gln
 435 440 445

 Ser Glu Ala Ala Met Pro Glu Pro Asp Phe Asp Ala Ile Gly Val Arg
 450 455 460

 Ala Ala Ala Phe Ser Asn Glu Ser
 465 470

<210> 31
 <211> 816
 <212> DNA
 <213> Methyloimonas 16a

<400> 31

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<210> 32
<211> 272
<212> PRT
<213> Methylomonas 16a

<400> 32

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Thr	Leu	Asn	Glu	Ala	Ala	Asn	Leu	Pro	Arg	Cys	Leu	Ala	Ala	Ile	Pro
				20				25						30	

Gln	Arg	Tyr	Pro	Val	Val	Ile	Leu	Asp	Ser	Gly	Ser	Ser	Asp	Asp	Thr
						35		40				45			

Leu	Ser	Ile	Ala	Glu	Gly	His	Gly	Cys	Lys	Ile	Tyr	Gln	Asn	Pro	Trp
						50		55				60			

Pro	Gly	Phe	Ala	Glu	Gln	Arg	Asn	Phe	Ala	Leu	Asn	Gln	Cys	Asp	Ile
						65		70			75			80	

Glu	Thr	Pro	Trp	Val	Leu	Phe	Val	Asp	Ala	Asp	Glu	Ile	Tyr	Pro	Gln
						85			90				95		

Val	Phe	Tyr	Gln	His	Phe	Asp	Ser	Gly	Met	Leu	Gln	Thr	Gly	Glu	Ile
						100			105			110			

Asp	Val	Leu	Met	Val	Pro	Ser	Ile	Leu	Phe	Leu	Arg	Gly	Lys	Arg	Leu
						115			120			125			

His	His	Ala	Pro	Gly	Tyr	Pro	Ile	Tyr	His	Pro	Arg	Leu	Val	Arg	Arg
						130			135			140			

Glu	Thr	Thr	Arg	Phe	Val	Arg	Asn	His	Thr	Gly	His	Gly	Glu	Ala	Val
						145		150			155			160	

Met	Asp	Ser	Cys	Arg	Ile	Gly	Tyr	Thr	Asp	Ile	Pro	Tyr	Asp	His	Tyr
						165			170			175			

Phe	Tyr	Asp	Gly	Glu	Ile	Ile	Gln	Trp	Met	His	Lys	His	Val	Asp	Lys
						180			185			190			

Ala Ala Gln Glu Val Arg Leu Lys Pro Thr Gln Gly Ala Leu Met Thr
195 200 205

Thr Arg Gly Arg Leu Ser Val Met Leu Gly Arg Ser Trp Ser Arg Ile
210 215 220

Leu Ala Arg Phe Val Tyr His Tyr Leu Leu Arg Gly Gly Phe Leu Asp
225 230 235 240

Gly Ala Ala Gly Leu Glu Phe Thr Leu Met Phe Thr Trp Tyr Glu Ala
245 250 255

Ser Ile Tyr Leu Gln Ala Lys Ala Ala Gln Ala Arg Gly Thr Ala
260 265 270

<210> 33

<211> 852

<212> DNA

<213> Methyloimonas 16a

<400> 33

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tatcacgcca acaaggacca ttacacgctg ggtaccgcgc gcatgctgaa atattccacc 660
ggtattggcg cctatatccg caaattcgcc aatcagcatg atccctataat cggctattac 720
atcctgcgca agatgctgat agccccgact ctgaaaatgc tgctggcctt gttgacgttc 780
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<210> 34

<211> 284

<212> PRT

<213> Methyloimonas 16a

<400> 34

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Leu Ile Val Ile Asp Gln Asn Gln Asp Gly Lys Ile Asp Arg Ile Ala
35 40 45

Glu Gln Tyr Ser Gln Cys Leu Asp Leu Lys His Val Lys Val Asn Phe
50 55 60

Thr Gly Asn Ala Arg Ala Arg Asp His Gly Ile Ala Leu Ala Gln Gly
65 70 75 80

Asp	Ile	Ile	Ala	Phe	Pro	Asp	Asp	Asp	Cys	Val	Tyr	Glu	Lys	Asp	Val
						85				90					95
Leu	Glu	Lys	Val	Val	Gly	Glu	Phe	Ala	Cys	Gln	Pro	Thr	Leu	Ser	Ile
						100			105				110		
Leu	Val	Ala	Gly	Ser	Tyr	Asp	Phe	Ser	Ala	Lys	His	Phe	Ser	Ile	Gly
						115			120				125		
Val	Asn	Ser	Arg	Lys	Ala	Arg	Tyr	Phe	Ser	Arg	Leu	Asn	Met	Met	Gly
						130			135			140			
Val	Glu	Phe	Thr	Gln	Phe	Phe	Ala	Leu	Ala	Arg	Ile	Asp	Arg	Arg	Gln
						145			150			155			160
Phe	Tyr	Leu	Asp	His	Asp	Phe	Gly	Ile	Gly	Ser	Lys	Tyr	Ala	Gly	Ala
						165			170			175			
Glu	Gly	Phe	Glu	Leu	Leu	Tyr	Arg	Leu	Leu	Arg	Ala	Gly	Gly	Arg	Ala
						180			185			190			
Phe	Tyr	Lys	Pro	Asp	Ile	Lys	Ile	Tyr	His	Ala	Asn	Lys	Asp	His	Tyr
						195			200			205			
Thr	Leu	Gly	Thr	Ala	Arg	Met	Leu	Lys	Tyr	Ser	Thr	Gly	Ile	Gly	Ala
						210			215			220			
Tyr	Ile	Arg	Lys	Phe	Ala	Asn	Gln	His	Asp	Pro	Tyr	Ile	Gly	Tyr	Tyr
						225			230			235			240
Ile	Leu	Arg	Lys	Met	Leu	Ile	Ala	Pro	Thr	Leu	Lys	Met	Leu	Leu	Ala
						245			250			255			
Leu	Leu	Thr	Phe	Asn	Pro	Gly	Lys	Leu	Ala	Tyr	Ser	Phe	Tyr	Asn	Leu
						260			265			270			
Val	Gly	Ile	Trp	Arg	Gly	Phe	Phe	Ala	Tyr	Gly	Arg				
						275			280						

<210> 35
 <211> 1194
 <212> DNA
 <213> Methyloimonas 16a

<400> 35															
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tcgtcgatg	aatccatcga	tgggtgcttg	aaaccggcg	acgtcaagct	gggcgcgaagc										180
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cgctattgcg	gctatctgca	gcgtgacgac	gtgatggcct	tgctggcgca	aagtcatttt										840

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 cggcgccatg ttcaacagca gctcgatccg gtcaaaactgg cggagcgcgt ctggcaagca 1140
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<210> 36
 <211> 398
 <212> PRT
 <213> Methylomonas 16a

<400> 36
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 Met Gly Leu Glu Met ala Leu Val Ser Ser Asp Glu Ser Ile Asp Gly
 35 40 45
 Cys Leu Lys Pro Ala Asp Val Lys Leu Gly Ala Ser Val Asp Val Asp
 50 55 60
 Leu Tyr Arg Cys Tyr Gly Phe Arg Arg Trp Gly Phe Gly Leu Gly Ala
 65 70 75 80
 Ile Pro Ser Leu Leu Arg Leu Cys Trp Gln Ala Pro Leu Val Tyr Ile
 85 90 95
 His Gly Val Ala Thr Trp Pro Ser Thr Leu Ala Ala Leu Phe Cys Cys
 100 105 110
 Leu Leu Arg Lys Pro Phe Met Val Ala Val His Gly Gly Leu Met Pro
 115 120 125
 Glu His Val Ala Leu Ile Lys Arg Lys Lys Arg His Lys Trp Trp Tyr
 130 135 140
 Tyr Lys Leu Leu Thr Phe Pro Thr Leu Arg Arg Ala Ile Ala Val His
 145 150 155 160
 Cys Thr Ser Asp Thr Glu Val Glu Gly Val Arg Asp Val Leu Gly Glu
 165 170 175
 Asn Ala Arg Val Leu Leu Val Pro Asn Gly Ile Asp Ser Arg Gly Val
 180 185 190
 Glu Glu Ala Pro Tyr Pro Ala Gly Glu Gly Met Gln Leu Cys Phe Leu
 195 200 205
 Gly His Val Gln Gln Glu Lys Gly Ile Asn Ala Phe Ile Arg Ala Trp
 210 215 220
 Leu Glu Val Arg Arg Pro Gly Asp Arg Leu Val Val Ala Gly Arg Ser
 225 230 235 240

Val	Asp	Gly	Asp	Tyr	Phe	Ala	Glu	Phe	Cys	Ser	Leu	Val	Glu	Arg	Ala
				245					250					255	
Asn	Gly	Ala	Ile	Arg	Tyr	Cys	Gly	Tyr	Leu	Gln	Arg	Asp	Asp	Val	Met
				260				265					270		
Ala	Leu	Leu	Ala	Gln	Ser	His	Phe	Leu	Val	Leu	Pro	Ser	Gly	Leu	Glu
				275				280					285		
Gln	Val	Gly	Gly	Met	Arg	Glu	Asn	Phe	Gly	Asn	Val	Val	Ala	Glu	Ala
				290			295			300					
Leu	Ala	Ala	Gly	Arg	Pro	Val	Leu	Val	Val	Arg	Gly	Leu	Ala	Trp	Asp
				305		310				315				320	
His	Leu	Pro	Ala	Leu	Asn	Ala	Gly	Leu	Val	Phe	Asp	Arg	Asp	Glu	Ala
				325				330			335				
Ala	Val	Gln	Ala	Val	Leu	Arg	Arg	Ala	Gln	Ala	Leu	Asp	Gln	Ala	Asp
				340			345					350			
Trp	Leu	Arg	Met	Ser	Gln	Ala	Gly	Arg	Arg	His	Val	Gln	Gln	Gln	Leu
				355			360					365			
Asp	Pro	Val	Lys	Leu	Ala	Glu	Arg	Val	Trp	Gln	Ala	Met	Thr	Ala	Ala
				370			375					380			
Val	Pro	Val	Asp	Glu	Ala	Lys	Val	Leu	Ala	Glu	Glu	Pro	Lys		
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<210> 37
<211> 951
<212> DNA
<213> Methyloimonas 16a

<400> 37
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<210> 38
<211> 317
<212> PRT
<213> Methyloimonas 16a

<400> 38

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20 25 30

Asp Arg Leu Leu Leu Ile Asp Ser Ser Ser Asp Asp Thr Val Ala
35 40 45

Leu Ala Arg Ala Arg Gly Phe Asp Ala His Val Ile Ala Lys Ala Ser
50 55 60

Phe Asn His Gly Gly Thr Arg Gln Ser Gly Val Asp Met Leu Val Asp
65 70 75 80

Met Asp Leu Ile Val Phe Leu Thr Gln Asp Ala Leu Leu Ala Asp Pro
85 90 95

Ser Ala Ile Glu Asn Leu Leu Gln Val Phe Val Asn Pro Gln Val Ala
100 105 110

Ala Ala Tyr Gly Arg Gln Leu Pro His Arg Asn Ala Gly Pro Ile Gly
115 120 125

Ala His Ala Arg Ile Phe Asn Tyr Pro Ala Gln Ser Gln Leu Arg Thr
130 135 140

Leu Gln Asp Arg Asp Arg Phe Gly Ile Lys Thr Val Phe Ile Ser Asn
145 150 155 160

Ser Phe Ala Ala Tyr Arg Arg Cys Ala Leu Met Gln Ile Gly Gly Phe
165 170 175

Pro Ala His Thr Ile Met Asn Glu Asp Thr Tyr Val Ala Gly Lys Met
180 185 190

Leu Leu Ser Gly Trp Ser Leu Ala Tyr Cys Ala Asp Ala Arg Val Phe
195 200 205

His Ser His Asp Tyr Ser Leu Leu Glu Glu Phe Arg Arg Tyr Phe Asp
210 215 220

Ile Gly Val Phe His Ala Gln Asn Pro Trp Leu Gln Gln Thr Phe Gly
225 230 235 240

Gly Ala Ser Gly Glu Gly Ala Arg Phe Val Leu Ser Glu Met Arg Tyr
245 250 255

Leu Ser Asn Thr Ala Pro Trp Leu Met Phe Ser Ala Phe Leu Arg Thr
260 265 270

Gly Leu Lys Trp Ala Gly Tyr Lys Leu Gly Gly Leu His Arg Gly Trp
275 280 285

Pro Leu Ala Leu Ser Arg Arg Leu Ser Leu His Lys Gly Tyr Trp Val
290 295 300

Ala Thr Glu Arg Glu Tyr Pro Asn Met Pro Gly Cys Arg
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<210> 39
<211> 1170
<212> DNA
<213> Methylomonas 16a

<220>
<223> ORF1

<220>
<223> nirF gene

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gtcatcaaca ccagcacgca caagatgctg agccgcacatcg aaggcctggg cgattttgtct 180
cacgcttcgg tgggtgttctc gcgtgtatcg cgctatgcct atgtattcg 240
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aaggatttca atatcgtaaa gaccctgc当地 ccgggttaagg ccgtgctgca catggagttc 1020
agcccgccgcg gcgaagccgt ctggatggcg gtgcgc当地 aggcacagggt aatggttac 1080
gacacggaca gttcaacga aaccgc当地 ctaccggccgc aaaagcccg cgcatctt 1140
ttcagtaatc gcgc当地atca gttgggctg 1170

<210> 40
<211> 390
<212> PRT
<213> Methylomonas 16a

<220>
<223> NirF

<400> 40
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Ser Ala Val Ala Asp Leu Arg Ala Thr Gly Asp Leu Gly Val Val Ile
      20          25           30

Glu Arg Glu Thr Gly Ser Val Gln Val Ile Asn Thr Ser Thr Pro Lys
      35          40           45

Met Leu Ser Arg Ile Glu Gly Leu Gly Asp Leu Ser His Ala Ser Val
      50          55           60

Val Phe Ser Arg Asp Gln Arg Tyr Ala Tyr Val Phe Gly Arg Asp Gly
      65          70           75           80

Gly Leu Ser Lys Ile Asp Leu Leu Gln Asp Lys Ile Glu Lys Arg Val
      85          90           95

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Val Gln Ala Gly Asn Ser Ile Gly Gly Ala Ile Ser Gln Asp Gly Lys
 100 105 110

 Val Ile Ala Val Ser Asn Tyr Thr Pro Gly Gly Val Lys Leu Phe Asp
 115 120 125

 Ala Glu Thr Leu Glu Gln Leu Ala Glu Ile Pro Ala Val Tyr Gly Asp
 130 135 140

 Asp Asn Gln Leu Ser Lys Val Val Gly Leu Val Asp Ala Pro Gly Gly
 145 150 155 160

 Arg Phe Val Cys Ser Leu Phe Glu Gly Asn Glu Ile Trp Leu Ile Asp
 165 170 175

 Ala Lys Asn Pro Arg Gln Pro Val Val Lys Lys Phe Lys Asp Ile Gly
 180 185 190

 Lys Arg Pro Tyr Asp Ala Leu Leu Thr Pro Asp Gly His Phe Tyr Ala
 195 200 205

 Ala Gly Leu Phe Gly Glu Lys Gly Leu Ala Leu Leu Asp Leu Trp Gln
 210 215 220

 Pro Glu Leu Gly Val Lys His Ile Leu Glu Asp Tyr Gly Lys Asp Asp
 225 230 235 240

 Glu Gln Leu Pro Val Tyr Lys Met Pro His Leu Glu Gly Trp Thr Val
 245 250 255

 Ala Gly Asp Leu Leu Phe Val Pro Ala Ile Gly Leu His Glu Val Leu
 260 265 270

 Val Ile Asp Lys His Asp Trp Glu Leu Val Lys Arg Ile Pro Val Val
 275 280 285

 Gly Gln Pro Val Phe Val Met Ser Arg Pro Asp Gly Arg Gln Val Trp
 290 295 300

 Val Asn Phe Ala Phe Pro Asp Asn Gln Thr Val Gln Val Ile Asp Val
 305 310 315 320

 Lys Asp Phe Asn Ile Val Lys Thr Leu Gln Pro Gly Lys Ala Val Leu
 325 330 335

 His Met Glu Phe Ser Pro Arg Gly Glu Ala Val Trp Met Ala Val Arg
 340 345 350

 Asp Glu Asp Arg Val Met Val Tyr Asp Thr Asp Ser Phe Asn Glu Thr
 355 360 365

 Ala Arg Leu Pro Ala Gln Lys Pro Ser Gly Ile Phe Phe Ser Asn Arg
 370 375 380

 Ala Asn Gln Leu Gly Leu
 385 390

<210> 41
 <211> 453

<212> DNA
 <213> *Methyloimonas* 16a

 <220>
 <223> ORF2

 <220>
 <223> *nirD* gene

 <400> 41
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 ccgacacccgt ttctggatat cgccgagcag cttggcggtca cggaaggcga agtgcgtggcg 120
 gcgtttcagg tggccgcga gcagcaaatg atcagccgca tcggccccgt gatgcgcggc 180
 aacgcccattcg gcaatagcgc cttggcggcg atggcggtgc cggagcagga tttggcccg 240
 gtcgcccgcct tggtgagcgc ctatccggaa gtcaatcata actatgagcg ggaaaaccgc 300
 ttcaatttgt ggttgtgtct gatgcgcctcc gatcataactc acttgcagcg ggtgattgcc 360
 gatatcgaga ctcaaaccgg ttatcaagcc atgctgttgc cgatgctggc cgattatttc 420
 atcaacctgg gtttgaact caatctgaac gac 453

 <210> 42
 <211> 151
 <212> PRT
 <213> *Methyloimonas* 16a

 <220>
 <223> NirD

 <400> 42
 Met Leu Ala Ser Leu His Lys His Leu Leu Asn Asp Tyr Gln Gln Asp
 1 5 10 15

 Phe Pro Leu Ser Pro Thr Pro Phe Leu Asp Ile Ala Glu Gln Leu Gly
 20 25 30

 Val Thr Glu Gly Glu Val Leu Ala Ala Phe Gln Val Leu Ala Glu Gln
 35 40 45

 Gln Met Ile Ser Arg Ile Gly Pro Val Ile Ala Pro Asn Ala Ile Gly
 50 55 60

 Asn Ser Ala Leu Val Ala Met Ala Val Pro Glu Gln Asp Leu Ala Arg
 65 70 75 80

 Val Ala Ala Leu Val Ser Ala Tyr Pro Glu Val Asn His Asn Tyr Glu
 85 90 95

 Arg Glu Asn Arg Phe Asn Leu Trp Phe Val Leu Ile Ala Ser Asp His
 100 105 110

 Thr His Leu Gln Arg Val Ile Ala Asp Ile Glu Thr Gln Thr Gly Tyr
 115 120 125

 Gln Ala Met Leu Leu Pro Met Leu Ala Asp Tyr Phe Ile Asn Leu Gly
 130 135 140

 Phe Glu Leu Asn Leu Asn Asp
 145 150

<210> 43
 <211> 504

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<212> DNA
<213> Methyloimonas 16a

<220>
<223> ORF3

<220>
<223> nirL gene

<400> 43
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cggccctatg ccgccatcgc cgcgaaattg gacatggacg aacaggacgt catcgcccga 120
ctgggacgtc tgaaaacgga aggttgatc aggcgctggg gcgtcggtt caagcacccgg 180
caacttaggtt atcgcgccaa tgcgatgatc gtgatggata ttccatgtga tcaagttcg 240
gaaatgggcc ggctgttcag ccagcacagc ttctgtcaatc tgtgttatcg ccgaccacgt 300
caaggcgagg tttggccgta taacctttat tgcatgatac acggaaaaaa tcgcgagacg 360
gtttgcagc aatgggccga tctgcaacaa agttgcggcc tggaaagctg tcggcacgag 420
attttattca gtctcgatc tttcaagcag cgtggggcta tttataaagc gccccgtgatt 480
gagccattgg agtttagtca tggaa 504

<210> 44
<211> 168
<212> PRT
<213> Methyloimonas 16a

<220>
<223> NirL

<400> 44
Met Asp Ala Leu Asp Tyr Arg Leu Ile Ala Ala Val Gln Ala Gly Leu
      1           5           10          15

Pro Leu Thr Ala Arg Pro Tyr Ala Ala Ile Ala Ala Lys Leu Asp Met
      20          25          30

Asp Glu Gln Asp Val Ile Ala Arg Leu Gly Arg Leu Lys Thr Glu Gly
      35          40          45

Leu Ile Arg Arg Trp Gly Val Val Val Lys His Arg Gln Leu Gly Tyr
      50          55          60

Arg Ala Asn Ala Met Ile Val Met Asp Ile Pro Asp Asp Gln Val Ala
      65          70          75          80

Glu Met Gly Arg Arg Val Ser Gln His Ser Phe Val Asn Leu Cys Tyr
      85          90          95

Arg Arg Pro Arg Gln Gly Glu Val Trp Pro Tyr Asn Leu Tyr Cys Met
      100         105         110

Ile His Gly Lys Asn Arg Glu Thr Val Leu Gln Gln Trp Ala Asp Leu
      115         120         125

Gln Gln Ser Cys Gly Leu Glu Ala Cys Arg His Glu Ile Leu Phe Ser
      130         135         140

Arg Arg Cys Phe Lys Gln Arg Gly Ala Ile Tyr Lys Ala Pro Val Ile
      145         150         155         160

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Glu Pro Leu Glu Phe Ser His Gly
165

<210> 45
<211> 441
<212> DNA
<213> *Methylomonas* 16a

<220>
<223> ORF4

<220>
<223> *nirG* gene

<400> 45
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tcgccttata gatatgtcgc cgagcagCTT ggtgtggCCG aggCGGAATT gctggagagg 120
ctgcaaacct tggtaaccca gggcgtttta tcgcgcTTT ggccgatgtA tcacGCCAG 180
caaattggcg gcgccttgac cttggcgCGC atgaagggtgc caggggagcg tttcgacgaa 240
attgcaggca tcgtcaacgg ctttccggag gtggcgcata actatgcgcg taaccacGCC 300
ttgaacatgt ggTTGTGTT ggcgaccgaa aagCCGGAAC aagtgcaggc ggtcatcgat 360
gccatcgAAC ggcaAAactgg cttgacggTC tataacatgc cgaaaatcaa ggaatattac 420
gtggcgttgc aactggaggc C 441

<210> 46
<211> 147
<212> PRT
<213> *Methylomonas* 16a

<220>
<223> NirG

<400> 46
Met Asp Asp Ile Asp Lys Ala Ile Ile Asn Arg Leu Gln Gln Gly Leu
1 5 10 15

Pro Ile Cys Glu Ser Pro Tyr Arg Tyr Val Ala Glu Gln Leu Gly Val
20 25 30

Ala Glu Ala Glu Leu Leu Glu Arg Leu Gln Thr Leu Leu Asn Gln Gly
35 40 45

Val Leu Ser Arg Phe Gly Pro Met Tyr His Ala Glu Gln Met Gly Gly
50 55 60

Ala Leu Thr Leu Ala Ala Met Lys Val Pro Gly Glu Arg Phe Asp Glu
65 70 75 80

Ile Ala Gly Ile Val Asn Gly Phe Pro Glu Val Ala His Asn Tyr Ala
85 90 95

Arg Asn His Ala Leu Asn Met Trp Phe Val Leu Ala Thr Glu Lys Pro
100 105 110

Glu Gln Val Gln Ala Val Ile Asp Ala Ile Glu Arg Gln Thr Gly Leu
115 120 125

Thr Val Tyr Asn Met Pro Lys Ile Lys Glu Tyr Tyr Val Gly Leu Gln
130 135 140

Leu Glu Ala

145

<210> 47

<211> 498

<212> DNA

<213> *Methylomonas* 16a

<220>

<223> ORF5

<220>

<223> *nirH* gene

<400> 47

atggactccg agccagtcaa aataatgate gacactatcg accgtcaaat catccaggcc 60
acccaggccg gcttgcgcgt ggtcgcggaa ccttatcagg ccgtcgccga gcaattgggc 120
atcacggctc aagaattgtat gctgcgcgtat gccgatatgc tggaagctgg catcattcgg 180
cgaggattgcgg cggtgcgcgaa tcattacaaa ctgggttatac gtcataacgg catgacggc 240
tgggatgtcg atgaccggca tgcgcacgc ctggggcagc gcgtcgccga attgccgttc 300
gtcagtcatt gctaccaacg gcctcgccat ttgccggatt ggccgtataa cctgttcgcg 360
atggtgcatg gcaagacgga acaagacgcc gaaaaacaaa ttgcgtgtat cgccgaattg 420
ttggcgagg attgctaccg gcacgcgggtg ctgtacagca ccaagattt gaagaaaacc 480
ggcttgagga ttgcgggg 498

<210> 48

<211> 166

<212> PRT

<213> *Methylomonas* 16a

<220>

<223> NirH

<400> 48

Met Asp Ser Glu Pro Val Lys Ile Met Ile Asp Thr Ile Asp Arg Gln
1 5 10 15

Ile Ile Gln Ala Thr Gln Ala Gly Leu Pro Leu Val Ala Glu Pro Tyr
20 25 30

Gln Ala Val Ala Glu Gln Leu Gly Ile Thr Ala Gln Glu Leu Met Leu
35 40 45

Arg Met Ala Asp Met Leu Glu Ala Gly Ile Ile Arg Arg Ile Ala Ala
50 55 60

Val Pro Asn His Tyr Lys Leu Gly Tyr Arg His Asn Gly Met Thr Val
65 70 75 80

Trp Asp Val Asp Asp Arg His Val Asp Ser Leu Gly Gln Arg Val Ala
85 90 95

Glu Leu Pro Phe Val Ser His Cys Tyr Gln Arg Pro Arg His Leu Pro
100 105 110

Asp Trp Pro Tyr Asn Leu Phe Ala Met Val His Gly Lys Thr Glu Gln
115 120 125

Asp Ala Glu Lys Gln Ile Ala Val Ile Ala Glu Leu Leu Gly Glu Asp
130 135 140

Cys Tyr Arg His Ala Val Leu Tyr Ser Thr Lys Ile Leu Lys Lys Thr
145 150 155 160

Gly Leu Arg Ile Ala Gly
165

<210> 49
<211> 1137
<212> DNA
<213> *Methylomonas* 16a

<220>
<223> ORF6

<220>
<223> *nirJ* gene

<400> 49
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cgcaaaccgt ccggccccgt ggtaatctgg aatctgatcc gtcgctgcaa cctgacttgc 120
aaggcattgtc ataccacgtc cgccgcacatc gatttccgg gtgaactgac gacgcccggaa 180
atttatgcgg ttagtggacga tttgaaagcc ttcaagggtgc cggtatttgat tctgtccggc 240
ggagagccgt tgctgcattcc ggatattttt ccgatttgc aacgcgcggc cgacatgggc 300
ttttacgtgg ccttgtccag caacggcaca ctgatgcaca aaaacaatat cgagcaaattc 360
gccgcgcatttcaata tattggcgta agtctggacg gcatgcgcga ggccgcacgac 420
aagttccgccc agaaggcaagg ctcttcgac gcctcgctgg ccggcatccg tttatgcccgc 480
gagcatggca tcaaggccgg cgtgcgcattc acgttgacgc gggacaacgc tcacgatttc 540
gatgccttgc tgcaagttgtat ggacgaggag gacatgcaca aattctatct gtcgcattctg 600
aattacggcg gcccggccaa taaaaaccgg aaagacgatg ccgagtttca gttgaccggc 660
aaggcatgg acgccttgc ttccggccgg ctgagctggg aacagcaagg cctacaccgc 720
gaagtggtca ccggcaacaa cgatgcccattt gccgtatatt tcctgcattt ggtcaaacgc 780
cgcttcccg agcgcgcgcgca gcatatccag gccaagttgc agcaatgggg cggcaatgct 840
tccggcgta acgttagccaa tatcgataat ctgggttaacg tgcatttttgc taccttttgg 900
tggcattaca acttggccag tgtccgcccag ccggccgttt ccgagatatg gcaggatgtg 960
tccgaccat ttagtggccgg gctgaaggcc tcgcccgcgcg cgctgaaaagg cccgtgcggc 1020
acctgtcatt atcaaagcat ttgcaacggc aatacccgcg tccgcgcggca acaactgacc 1080
ggcgattttt gggctgaaga tccaggctgc tacctggatg acgaggaagt tttcagc 1137

<210> 50
<211> 379
<212> PRT
<213> *Methylomonas* 16a

<220>
<223> Nir J

<400> 50
Met Phe Arg Leu Ser Gln Tyr Met Arg Glu Leu Val His Ser Thr Pro
1 5 10 15

Leu Gly Lys Pro Arg Lys Pro Ser Gly Pro Val Val Ile Trp Asn Leu
20 25 30

Ile Arg Arg Cys Asn Leu Thr Cys Lys His Cys Tyr Thr Thr Ser Ala
35 40 45

Asp Ile Asp Phe Pro Gly Glu Leu Thr Thr Pro Glu Ile Tyr Ala Val
50 55 60

Met Asp Asp Leu Lys Ala Phe Lys Val Pro Val Leu Ile Leu Ser Gly
 65 70 75 80

Gly Glu Pro Leu Leu His Pro Asp Ile Phe Pro Ile Ser Gln Arg Ala
 85 90 95

Ser Asp Met Gly Phe Tyr Val Ala Leu Ser Ser Asn Gly Thr Leu Ile
 100 105 110

Asp Lys Asn Asn Ile Glu Gln Ile Ala Ala Ile Asp Tyr Gln Tyr Ile
 115 120 125

Gly Val Ser Leu Asp Gly Met Arg Glu Ala His Asp Lys Phe Arg Gln
 130 135 140

Lys Gln Gly Ser Phe Asp Ala Ser Leu Ala Gly Ile Arg Leu Cys Arg
 145 150 155 160

Glu His Gly Ile Lys Ala Gly Val Arg Phe Thr Leu Thr Arg Asp Asn
 165 170 175

Ala His Asp Phe Asp Ala Leu Leu Gln Leu Met Asp Glu Glu Asp Ile
 180 185 190

Asp Lys Phe Tyr Leu Ser His Leu Asn Tyr Gly Gly Arg Gly Asn Lys
 195 200 205

Asn Arg Lys Asp Asp Ala Glu Phe Gln Leu Thr Arg Lys Val Met Asp
 210 215 220

Ala Leu Phe Glu Lys Ala Leu Ser Trp Glu Gln Gln Gly Leu His Arg
 225 230 235 240

Glu Val Val Thr Gly Asn Asn Asp Ala Asp Ala Val Tyr Phe Leu His
 245 250 255

Trp Val Lys Arg Arg Phe Pro Glu Arg Ala Glu His Ile Gln Ala Lys
 260 265 270

Leu Gln Gln Trp Gly Gly Asn Ala Ser Gly Val Asn Val Ala Asn Ile
 275 280 285

Asp Asn Leu Gly Asn Val His Pro Asp Thr Phe Trp Trp His Tyr Asn
 290 295 300

Leu Gly Ser Val Arg Gln Arg Pro Phe Ser Glu Ile Trp Gln Asp Val
 305 310 315 320

Ser Asp Pro Leu Met Ala Gly Leu Lys Ala Ser Pro Arg Pro Leu Lys
 325 330 335

Gly Arg Cys Gly Thr Cys His Tyr Gln Ser Ile Cys Asn Gly Asn Thr
 340 345 350

Arg Val Arg Ala Gln Gln Leu Thr Gly Asp Phe Trp Ala Glu Asp Pro
 355 360 365

Gly Cys Tyr Leu Asp Asp Glu Glu Val Phe Ser
 370 375

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<210> 51
<211> 2760
<212> DNA
<213> Methyloimonas 16a

<220>
<223> ORF7

<220>
<223> nasA gene

<400> 51
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tccaatttcg gcccactgtg ctccaagggc gggcgctgg gtgataccgt cggcttgaa 180
ggccgccttt tatacccgaa aatcgatggc cggcgctgg attggccac ggtgctggac 240
cgatcgccg ctaaattcaa tgcgatcatt gccgagcacg gccccgacgc ggtggcgaaa 300
tatgtgtccg gacagttgtt gaccgaggat tattatgtcg ccaacaatt gatgaagggc 360
ttcatcggtt cggcgaatat cgataccaaat tccaggctgt gcatgtcctc ggcggtagtc 420
gttacaagc gtgcgttcgg cggcgatgcg gtgcctgtt atttcgagga tctggAACGG 480
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cgcatcgctc aggccaagat agacaatccg gcgctgaaaa tcgtactaat agaccggcgt 600
caaaccagca gtcgcgatataat cggcgatccg catctggcca tcaagccccgg catggacggc 660
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gattttacccg ttctggccaa ccgttggcgc gtggcggcgc acgatctggc gcaactgttt 840
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gtgcgcatcg cggcttggc accttgcgtt caagcgatgg tattgacgaa aatgcatttgc 2160
gacatcgacg attgcataa ccacgtcaaa ataaggggcc atggcttttgc ggcgtatcat 2220
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ggggcgccca aacccaatga ttgcgtggaa tatctcgacc tggccgtcg cgttaccgc 2340
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cgcttcaacc tgctcagcg cgtgcgcgcg caaggggaaa tcgatcgcc caaaacgatc 2520
tgctcctgtt tcacacgtcgg cggaaaaacc atcgtcgaag ccattcaac cgcacatttgc 2580
agctgtgtaa cagatatagg caactgcctg catgcggggaa cgggttgcgtt ttcgtgttta 2640
ccggaattaa aaagcattttt ggcccacgc aaaacgatcg atccctgcctc gtcgtccatt 2700
cagccaaactc aaatcccggc ggcacatcgag gggaaaggagg aagccctttt ttcaggtcaa 2760

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<210> 52
<211> 920
<212> PRT
<213> Methylomonas 16a

<220>
<223> NasA

<400> 52
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Cys Gly Ile Glu Ala Arg Val Leu Asp Ala Glu Asn His Val Val Asn
20 25 30

Ile Ala Gly Asp Pro Gln His Gln Ser Asn Phe Gly Arg Leu Cys Ser
35 40 45

Lys Gly Ala Ala Leu Gly Asp Thr Val Gly Leu Glu Gly Arg Leu Leu
50 55 60

Tyr Pro Glu Ile Asp Gly Arg Arg Val Asp Trp Pro Thr Val Leu Asp
65 70 75 80

Arg Ile Ala Ala Lys Phe Asn Ala Ile Ile Ala Glu His Gly Pro Asp
85 90 95

Ala Val Ala Phe Tyr Val Ser Gly Gln Leu Leu Thr Glu Asp Tyr Tyr
100 105 110

Val Ala Asn Lys Leu Met Lys Gly Phe Ile Gly Ser Ala Asn Ile Asp
115 120 125

Thr Asn Ser Arg Leu Cys Met Ser Ser Ala Val Val Gly Tyr Lys Arg
130 135 140

Ala Phe Gly Ala Asp Ala Val Pro Cys Asn Phe Glu Asp Leu Glu Arg
145 150 155 160

Ala Asp Leu Ile Val Leu Val Gly Ser Asn Ala Ala Trp Cys His Pro
165 170 175

Ile Ala Phe Gln Arg Met Arg Gln Ala Lys Ile Asp Asn Pro Ala Leu
180 185 190

Lys Ile Val Leu Ile Asp Pro Arg Gln Thr Ser Ser Cys Asp Ile Ala
195 200 205

Asp Arg His Leu Ala Ile Lys Pro Gly Met Asp Gly Leu Leu Phe Asn
210 215 220

Gly Leu Leu Val Tyr Leu Ala Glu Thr Gly Ala Leu Asp Gln Asp Tyr
225 230 235 240

Ile Glu Arg His Cys Glu Gly Phe Ala Glu Ala Leu Ala Thr Ala Arg
245 250 255

Ala Ser Ala Ala Asp Phe Thr Val Leu Ala Asn Arg Cys Gly Val Ala
260 265 270

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Ala His Asp Leu Ala Gln Leu Phe Ala Trp Phe Ala Gly Leu Asp Lys
 275 280 285

 Val Val Thr Val Tyr Ser Gln Gly Ile Asn Gln Ser Ser Ser Gly Ser
 290 295 300

 Asp Lys Cys Asn Ala Ile Ile Asn Cys His Leu Ala Ser Gly Lys Ile
 305 310 315 320

 Gly Lys Pro Gly Cys Gly Pro Phe Ser Phe Thr Gly Gln Pro Asn Ala
 325 330 335

 Met Gly Gly Arg Glu Val Gly Gly Leu Ala Asn Met Leu Ala Ala His
 340 345 350

 Met Asp Leu Glu Asn Pro Ala His Val Asp Arg Val Ala Arg Phe Trp
 355 360 365

 Gln Thr Asp Ser Val Ala Arg Lys Pro Gly Leu Lys Ala Val Glu Ile
 370 375 380

 Phe Asp Ala Ile Ala Asp Gly Arg Ile Lys Ala Leu Trp Ile Met Ala
 385 390 395 400

 Thr Asn Pro Val Val Ser Met Pro Asp Ala Asp Lys Val Ile Glu Ala
 405 410 415

 Leu Lys Gln Cys Glu Phe Leu Leu Val Ser Asp Cys Ile Ala Asn Thr
 420 425 430

 Asp Thr Val Glu Leu Ala His Val Lys Leu Pro Ala Thr Gly Trp Ser
 435 440 445

 Glu Lys Asp Gly Thr Val Thr Asn Leu Glu Arg Arg Ile Ser Arg Gln
 450 455 460

 Arg Pro Leu Phe Gln Pro Ser Gly Glu Ala Lys Pro Asp Trp Trp Ile
 465 470 475 480

 Val Ser Gln Val Ala Lys Arg Met Gly Phe Ala Gly Phe Asp Tyr Arg
 485 490 495

 Asn Ser Ala Glu Ile Phe Lys Glu His Ala Ala Leu Ser Gly Phe Glu
 500 505 510

 Asn Asp Ala Ala Gln Gly Gly Arg Asp Phe Asp Ile Ser Gly Leu Ala
 515 520 525

 Thr Leu Asp Gln Ala Gln Phe Asp Ala Leu Val Pro Ile Gln Trp Pro
 530 535 540

 Val Thr Gly Lys Thr Gln Gly Gly Thr Ala Arg Leu Phe Glu Asp Gly
 545 550 555 560

 Arg Phe Phe Thr Asp Thr Gly Lys Ala Arg Phe Ile Ala Leu Glu Pro
 565 570 575

 Arg Ser Pro Met His Ala Pro Thr Pro Asp Tyr Pro Leu Val Leu Asn
 580 585 590

Thr Gly Arg Ile Arg Asp Gln Trp His Thr Met Thr Arg Thr Ala Leu
 595 600 605
 Ser Ala Lys Leu Asn Gln His Lys Pro Glu Pro Phe Val Glu Ile His
 610 615 620
 Pro Gln Asp Ala Leu Arg Trp Gly Leu Lys Ala Asn Ala Leu Ala Arg
 625 630 635 640
 Ile Glu Ser Arg Trp Gly Gly Met Leu Ala Arg Val Asp Val Ser Glu
 645 650 655
 Ala Gln Gln Pro Gly Ser Val Phe Val Pro Met His Trp Thr Ala Gln
 660 665 670
 Leu Ser Ser His Gly Arg Val Gly Ala Val Val Asn Pro Val Val Asp
 675 680 685
 Pro Leu Ser Gly Gln Pro Glu Ser Lys Gln Thr Pro Val Arg Ile Ala
 690 695 700
 Ala Trp Ala Pro Cys Trp Gln Ala Met Val Leu Thr Lys Met Pro Leu
 705 710 715 720
 Asp Ile Asp Asp Cys Glu Tyr His Val Lys Ile Arg Gly His Gly Phe
 725 730 735
 Trp Arg Tyr His Leu Ala Asp Gln Ser Gln Arg Pro Asp Leu Pro Ala
 740 745 750
 Trp Gly Arg Gly Ile Val Gly Arg Gly Ala Ala Lys Pro Asn Asp Cys
 755 760 765
 Val Glu Tyr Leu Asp Leu Ala Ala Gly Asp Tyr Arg Phe Ala Glu Met
 770 775 780
 Arg Asp Gln Thr Leu His Ala Cys Met Phe Ile Thr His Asn Gly Glu
 785 790 795 800
 Leu Pro Asp Pro Gly Trp Leu Ala Ser Leu Phe Gly Lys Pro Arg Leu
 805 810 815
 Thr Arg Lys Glu Arg Phe Asn Leu Leu Ser Gly Val Pro Pro Gln Gly
 820 825 830
 Glu Ile Asp Ser Gly Lys Thr Ile Cys Ser Cys Phe Asn Val Gly Glu
 835 840 845
 Lys Thr Ile Val Gln Ala Ile Gln Thr Arg His Leu Ser Cys Val Thr
 850 855 860
 Asp Ile Gly Asn Cys Leu His Ala Gly Thr Gly Cys Gly Ser Cys Leu
 865 870 875 880
 Pro Glu Leu Lys Ser Ile Leu Ala His Ala Lys Thr Ile Asp Pro Ala
 885 890 895
 Ser Leu Pro Ile Gln Pro Thr Gln Ile Pro Pro Ala Ser Glu Gly Lys
 900 905 910

Glu Glu Ala Phe Phe Ser Gly Gln
 915 920

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 <211> 642
 <212> DNA
 <213> *Methylomonas* 16a

<220>
 <223> ORF8

<220>
 <223> norC gene

<400> 53
 atggcaacga aaccgaacat tcacatcaac ctggaggctcg tcatgactga gcaagtcccg 60
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 gtgttgcgtgg tgatcttgac ctgcgactcg ctggcgaaga tttccgctgg cggccccagg 180
 gtgcggcct tcgacgtcat caacaaagac gtcagttacc gtttcgacaa ggaaaaaccaa 240
 cgctaccaac cagtgatcggt cgacgacgccc cctctgtttg gcaaaaacct gagcgaggaa 300
 gaagccgaaa aactggtcga cctggcgaag aaaaccgtgc aggccaagaa ctgcatgaac 360
 tgccataaccc tgctcggcaa tggcgcttat tatgcgccc actgtaccaa ggcctggctg 420
 gaccagggt ggatcgccaa ggagtcgcgc gagcaaatga tggtcaattt cctgctcgat 480
 cccgagaaaa atgcccgcac ctgcgctcc aaccgcaaga tgccgaatct cgacatcacg 540
 caacaggagg ccgagggcat cgtcgccctt ttgaaatgga tggcatccat cgacaccaat 600
 ggttttccgc ataatttcat cgcgctggc gaagaggaca aa 642

<210> 54
 <211> 214
 <212> PRT
 <213> *Methylomonas* 16a

<220>
 <223> NorC

<400> 54
 Met ala Thr Lys Pro Asn Ile His Ile Asn Leu Glu Val Val Met Thr
 1 5 10 15

Glu Gln Val Pro Arg Trp Ala Ser Glu Thr Phe Trp Lys Lys Thr Ala
 20 25 30

Ile Trp Val Thr Gly Gly Ser Phe Val Leu Leu Val Ile Leu Thr Phe
 35 40 45

Asp Ser Leu Ala Lys Ile Ser Ala Gly Gly Pro Arg Val Pro Ala Phe
 50 55 60

Asp Val Ile Asn Lys Asp Val Ser Tyr Arg Phe Asp Lys Glu Lys Gln
 65 70 75 80

Arg Tyr Gln Pro Val Ile Gly Asp Asp Ala Pro Leu Phe Gly Lys Thr
 85 90 95

Leu Ser Glu Glu Glu Ala Glu Lys Leu Val Asp Leu Gly Lys Lys Thr
 100 105 110

Val Gln Ala Lys Asn Cys Met Asn Cys His Thr Leu Leu Gly Asn Gly
 115 120 125

Ala Tyr Tyr Ala Pro Asp Leu Thr Lys Ala Trp Leu Asp Gln Gly Trp
130 135 140

Ile Ala Lys Glu Ser Arg Glu Gln Met Met Val Asn Phe Leu Leu Asp
145 150 155 160

Pro Glu Lys Asn Ala Arg Thr Phe Gly Ser Asn Arg Lys Met Pro Asn
165 170 175

Leu Asp Ile Thr Gln Gln Glu Ala Glu Gly Ile Val Ala Phe Leu Lys
180 185 190

Trp Met Ala Ser Ile Asp Thr Asn Gly Phe Pro His Asn Phe Ile Ala
195 200 205

Leu Gly Glu Glu Asp Lys
210

<210> 55

<211> 1503

<212> DNA

<213> *Methylomonas* 16a

<220>

<223> ORF9

<220>

<223> norB gene

<400> 55

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ttcacccgtcg ccatggtgct gttcatggcg caatttgcgt tcggcctgct ggccggcctg 180
caatttcattt tcccgagttt tttatacgaa atcctggatt tcaacgtcaa ccgcattgtg 240
cacatcaatg ccatggtggt gtggatgctg tacggcttt tgggctcggt gtactggttt 300
cttggaaagacg agagcggcgt cgagatcgcc ggcttgaat gggggcaact ggcgttttgg 360
gtgctgaccgg gtgcgggtcgc gctggctgtg ctgggttatt tgttcatcca gatcggcgcc 420
ggcaacgaca cttcgctgtg gctgatcaac gaaggccgca aatacatcgaa agccccgcgc 480
tgggcccaca tcggcattcggt cgccgtggta ttgaccttct tttacaacgt cgccgccacc 540
tttcgccaag gcaaatggtc cggcattgccc ggcgtgttga ccctggatct ggtggccctg 600
gcccggcttgt atctggccgg catgttctac gtcaccaata ttccggtcga ccaatactgg 660
tgggtggggg tgatccatct atgggtcgaa gcgacctggg aagtgtggg tggctgcattc 720
atggccttggaa gcctgatgaa gctgctgggc gtgcggccccc aggtcgtaca aacttgggtt 780
tacatcgaaat ttgcattgtat gttcggttcc ggcatttttgc gcctgggtca tcactatattc 840
tggatcgca cgcggaaata ctggttcagc atcggcggtc ttcttcggc gctggaaaccg 900
attccgcgtgg tagcaatggc cgtgcattcc atttacgatt ccggcgtcga caagttaaa 960
aacagcaatc accccgcctt ggcctggatc atcgcccata ctttcggca cttcctggc 1020
gcccggcttt ggggattcat gcacacgctg cgcggaaatca acctgtacac ccacggcaccg 1080
caatggtcgg cctcgacgg ccacctggcc ttcttcggc cctatgcgc catcaacatc 1140
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tggcgcatgg tattcggctt gatgacggcc gtccggcgcc gcctgttgc ctggactt 1440
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gaa 1503

<210> 56

<211> 501

<212> PRT
<213> *Methylomonas* 16a

<220>
<223> NorB

<400> 56
Met Thr Leu Gln Ala Tyr Gln Glu Lys Ala Ala Val Cys Trp Ala Gly
1 5 10 15

Cys Lys Gln Arg His Ala Asp Phe Met Ala Asn Pro His Leu Thr Gly
20 25 30

Gly Gln Lys Leu Ala Val His Tyr Phe Thr Val Ala Met Val Leu Phe
35 40 45

Met Ala Gln Leu Leu Phe Gly Leu Leu Ala Gly Leu Gln Phe Ile Phe
50 55 60

Pro Ser Phe Leu Tyr Glu Ile Leu Asp Phe Asn Val Asn Arg Met Val
65 70 75 80

His Ile Asn Ala Met Val Val Trp Met Leu Tyr Gly Phe Leu Gly Ser
85 90 95

Val Tyr Trp Phe Leu Glu Asp Glu Ser Gly Val Glu Ile Val Gly Leu
100 105 110

Lys Trp Gly Gln Leu Ala Phe Trp Val Leu Thr Gly Ala Val Ala Leu
115 120 125

Val Val Leu Val Tyr Leu Phe Ile Gln Ile Gly Ala Gly Asn Asp Thr
130 135 140

Ser Leu Trp Leu Ile Asn Glu Gly Arg Glu Tyr Ile Glu Ala Pro Arg
145 150 155 160

Trp Ala Asp Ile Gly Ile Val Ala Val Val Leu Thr Phe Phe Tyr Asn
165 170 175

Val Ala Ala Thr Phe Ala Lys Gly Lys Trp Ser Gly Ile Ala Gly Val
180 185 190

Leu Thr Leu Asp Leu Val Ala Leu Ala Gly Leu Tyr Leu Ala Gly Met
195 200 205

Phe Tyr Val Thr Asn Ile Ser Val Asp Gln Tyr Trp Trp Trp Trp Val
210 215 220

Ile His Leu Trp Val Glu Ala Thr Trp Glu Val Leu Val Gly Cys Ile
225 230 235 240

Met Ala Trp Ser Leu Met Lys Leu Leu Gly Val Arg Arg Gln Val Val
245 250 255

Gln Thr Trp Leu Tyr Ile Glu Val Ala Leu Met Phe Gly Ser Gly Ile
260 265 270

Leu Gly Leu Gly His His Tyr Phe Trp Ile Gly Thr Pro Glu Tyr Trp
275 280 285

Phe Ser Ile Gly Gly Phe Phe Ser Ala Leu Glu Pro Ile Pro Leu Val
 290 295 300

 Ala Met Val Val His Ser Ile Tyr Asp Ser Gly Val His Lys Phe Lys
 305 310 315 320

 Asn Ser Asn His Pro Ala Leu Ala Trp Ile Ile Ala His Thr Phe Gly
 325 330 335

 Asn Phe Leu Gly Ala Gly Val Trp Gly Phe Met His Thr Leu Pro Gln
 340 345 350

 Ile Asn Leu Tyr Thr His Gly Thr Gln Trp Ser Ala Ser His Gly His
 355 360 365

 Leu Ala Phe Phe Gly Ala Tyr Ala Thr Ile Asn Ile Ala Phe Phe Tyr
 370 375 380

 Leu Ala Ala Gln Gln Ala Arg Gly Asn Val Trp Met Gly Gly Asp Leu
 385 390 395 400

 Ile Asn Gly Trp Arg Trp Lys Ala Ala Ala Ile Leu Leu Asn Leu Gly
 405 410 415

 Val Leu Gly Met Thr Val Ala Leu Leu Ile Ala Gly Tyr Glu Gln Ser
 420 425 430

 Phe Ile Glu Arg Ala Val Glu Gly Ser Thr Trp Ala Gly Tyr Phe Ala
 435 440 445

 Ala Gln Asn His Pro Trp Phe Met Gln Ala Met Val Trp Arg Met Val
 450 455 460

 Phe Gly Leu Met Thr Ala Val Gly Gly Leu Leu Phe Trp Asp Leu
 465 470 475 480

 Leu Glu Ile Gly Lys Gly Glu Gln Arg Pro Ala Ala Val Ile Ala Gly
 485 490 495

Gly Thr Val Ala Glu
500

<210> 57
<211> 2253
<212> DNA
<213> *Methyloomonas* 16a

<220>
<223> ORF10

<220>
<223> norZ gene

<400> 57
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ctgggcttg cagggctgat cgtcatcaca tcgctggcct atcgtaatgc tccgcccatt 120
ccggccccaaa tcgttcatgc acaagggttt cgcctgttt ccgggtacga aatcaaagaa 180
ggccaggcta tctttctcaa atacgggttg atgaacaacg gcagtatctg gggtcatggc 240
gcataacttgg ggccagatta ttcggccgag gcattgcacc gaatcggcga gaacaccgccc 300

actatcattg cccagcagca ataccaacag ccacttcct cactcacgcc cgccaattg 360
 gcccgtgt atgcacaaac cgcaatcgag ctaaagacca atcattatga tgccgccagc 420
 gcaacgttgc gtctgaccgt gccggagaca tccgcctatc gtaaggcatcgat cgcttattgg 480
 acggattatt tcctgaatcc tgaacggaat ggcggactca aacgtggatt gatcagcgat 540
 ccgactgaac tgcgccttc atcacatgga ctgcctggc ctcggtgcc 600
 aaccgccccg gcgagaacta ctctacacc aacaatttc catacgaccc cagcgtcgcc 660
 aatatgccccg ttcccggtgc gctgttatgg agtgcgttga gccttatcgat gctgctggcc 720
 ggtattggaa tcgtacttct gatgttgaa aaattcgatt atcttggctg gattagcaca 780
 ggacatcatg tacatcctca tctgttgctt gggcaagcca gtgcggctca actagactg 840
 gtgaaatttt tcgtggtggt ggcgctgctg tttcttgctc agaccttggt gggcggtgca 900
 acggcgcaact atcgccgca tccaggcagt ttttacggcc tttagctggaa gaagctattt 960
 cccagcaatc tcatgcgcac ctggcatcta caaaccggg ttttctggat tgccaccgct 1020
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 ggttggaaat acctggagct cggccgtctg tggcagtacc tgcttatcgat cggctctgctg 1260
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 ggcatgtgg cactggact gatggatttgc gtgttgcgcc agaccagctc cgatttgcgc 1980
 tgggtcgaca tcgagaaata cgtaagggtc ggattttggg gctccaatgt tggcctggct 2040
 ctgtatgttac tcatgagctt gttccccagt ggcgttgc aagttggaa tgcgttccag 2100
 catggataact ggcatgcgcg cagccttgc tacatcgccgca gcgaaaggc ggcctgatc 2160
 gaatggctac gtctgcccgg tgatctggta tttatcctgt ttggcgccat accgttggca 2220
 atcgcatcca tcaaaggctg gctggatgtg cat 2253

<210> 48
 <211> 751
 <212> PRT
 <213> *Methylomonas* 16a

<220>
 <223> NorZ

<400> 48
 Met Thr Lys Thr Pro Asp Leu Ser Pro Trp Trp Leu Arg Thr Val Leu
 1 5 10 15

Ile Val Met Val Leu Gly Phe Ala Gly Leu Ile Val Ile Thr Ser Leu
 20 25 30

Ala Tyr Arg Asn Ala Pro Pro Ile Pro Ala Gln Ile Val Asp Ala Gln
 35 40 45

Gly Val Arg Leu Phe Ser Gly Asp Glu Ile Lys Glu Gly Gln Ala Ile
 50 55 60

Phe Leu Lys Tyr Gly Leu Met Asn Asn Gly Ser Ile Trp Gly His Gly
 65 70 75 80

Ala Tyr Leu Gly Pro Asp Tyr Ser Ala Glu Ala Leu His Arg Ile Gly
 85 90 95

Glu Asn Thr Ala Thr Ile Ile Ala Gln Gln Gln Tyr Gln Gln Pro Leu
 100 105 110
 Ser Ser Leu Thr Pro Gly Gln Leu Ala Ala Val Tyr Ala Gln Thr Ala
 115 120 125
 Val Glu Leu Lys Thr Asn His Tyr Asp Ala Ala Ser Ala Thr Leu Arg
 130 135 140
 Leu Thr Val Pro Glu Thr Ser Ala Tyr Arg Lys Gln Ile Ala Tyr Trp
 145 150 155 160
 Thr Asp Tyr Phe Leu Asn Pro Glu Arg Asn Gly Gly Leu Lys Arg Gly
 165 170 175
 Leu Ile Ser Asp Pro Thr Glu Leu Arg Gln Phe Thr Ala Phe Ile Thr
 180 185 190
 Trp Thr Ala Trp Ala Ser Val Ala Asn Arg Pro Gly Glu Asn Tyr Ser
 195 200 205
 Tyr Thr Asn Asn Phe Pro Tyr Asp Pro Ser Val Gly Asn Met Pro Val
 210 215 220
 Pro Gly Ala Leu Leu Trp Ser Ala Leu Ser Leu Ile Val Leu Leu Ala
 225 230 235 240
 Gly Ile Gly Ile Val Leu Leu Met Phe Gly Lys Phe Asp Tyr Leu Gly
 245 250 255
 Trp Ile Ser Thr Gly His His Val His Pro His Leu Leu Pro Gly Gln
 260 265 270
 Ala Ser Ala Gly Gln Leu Ala Leu Val Lys Phe Phe Val Val Val Ala
 275 280 285
 Leu Leu Phe Leu Ala Gln Thr Leu Val Gly Gly Ala Thr Ala His Tyr
 290 295 300
 Arg Ala Asp Pro Gly Ser Phe Tyr Gly Leu Glu Leu Glu Lys Leu Phe
 305 310 315 320
 Pro Ser Asn Leu Met Arg Thr Trp His Leu Gln Thr Ala Val Phe Trp
 325 330 335
 Ile Ala Thr Ala Phe Val Ala Ala Leu Phe Leu Gly Arg Ser Leu
 340 345 350
 Arg Asn Asp Glu Pro Arg Trp Phe Ala Gly Trp Val His Leu Leu Phe
 355 360 365
 Gly Ala Phe Ala Val Val Ile Gly Gly Ser Leu Leu Gly Glu Trp Ala
 370 375 380
 Gly Ile Ser Gln Met Leu Asp Gln Trp Trp Phe Trp Leu Gly Asn Gln
 385 390 395 400
 Gly Trp Glu Tyr Leu Glu Leu Gly Arg Leu Trp Gln Tyr Leu Leu Ile
 405 410 415

Ala Gly Leu Leu Ala Trp Phe Thr Leu Leu Phe Lys Leu Leu Gln Pro
 420 425 430

 Asp Thr Leu Asn Asp Ser Glu Ala Lys Pro Leu Val Arg Leu Phe Leu
 435 440 445

 Leu Ala Ser Leu Ala Ile Pro Leu Phe Tyr Ile Pro Ala Leu Phe Phe
 450 455 460

 Gly Ala Lys Thr Asn Phe Thr Val Val Asp Thr Trp Arg Phe Trp Ile
 465 470 475 480

 Ile His Leu Trp Val Glu Gly Phe Phe Glu Phe Ala Thr Thr Leu
 485 490 495

 Val Ala Leu Leu Phe Tyr Gln Leu Gly Leu Thr Gln Arg Asn Val Ala
 500 505 510

 Leu Arg Val Ile Tyr Leu Asp Ala Ile Leu Tyr Phe Val Gly Gly Leu
 515 520 525

 Ile Gly Thr Gly His His Trp Tyr Phe Thr Gly Gln Ser Ser Val Asn
 530 535 540

 Met ala Leu Ser Ala Met Val Ser Val Leu Glu Val Val Pro Leu Thr
 545 550 555 560

 Leu Leu Thr Leu Asp Ala Trp Asp Phe Val Arg Thr Thr Arg Ala Asp
 565 570 575

 Cys Asp Val Cys Gly Lys Pro Val Ala Ile Pro His Lys Trp Thr Phe
 580 585 590

 Tyr Phe Leu Met ala Val Gly Phe Trp Asn Phe Val Gly Ala Gly Ile
 595 600 605

 Phe Gly Phe Leu Ile Asn Leu Pro Ile Val Ser Tyr Tyr Glu Val Gly
 610 615 620

 Thr Gln Leu Thr Pro Asn His Gly His Ala Ala Met Met Gly Val Phe
 625 630 635 640

 Gly Met Leu Ala Leu Ala Leu Met Val Phe Val Leu Arg Gln Thr Ser
 645 650 655

 Ser Asp Leu Arg Trp Val Asp Ile Glu Lys Tyr Val Arg Val Gly Phe
 660 665 670

 Trp Gly Ser Asn Val Gly Leu Ala Leu Met Leu Ile Met Ser Leu Phe
 675 680 685

 Pro Ser Gly Val Leu Gln Val Trp Asp Val Val Gln His Gly Tyr Trp
 690 695 700

 His Ala Arg Ser Leu Asp Tyr Ile Gly Ser Glu Arg Ser Arg Leu Ile
 705 710 715 720

 Glu Trp Leu Arg Leu Pro Gly Asp Leu Val Phe Ile Leu Phe Gly Ala
 725 730 735

Ile Pro Leu Ala Ile Ala Ser Ile Lys Gly Trp Leu Asp Val His
740 745 750

<210> 59
<211> 1581
<212> DNA
<213> *Methylomonas* 16a

<220>
<223> ORF11

<220>
<223> norS gene

<400> 59

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gcgttactgt cgtccggcgc ggtgctggcg aaatccgaca gcccacacga catctacatg 120
gataattgcg ccagctgcca cggcgccggat cacgggtggct atctggcgcc agccttgaat 180
gccgataacct tgaagggtcg tagccctacg gcgttgcgtta ccatcgtcat ggccggcagc 240
ttcgataacgc tgatgcctcc cttctacggc aaactgagacg acgacgagat tcgcggcgtg 300
atcaaggcatt tgcaggaaac cccgaaacag cccgaatccgg cctggaccat cgacgacatg 360
aagaagtcc tgaagggtta cgtcaaggat gagagcaccc tgcctggcaa gccgacttcc 420
caaatcgata acatcgataa tctgatcgcc gtggccggcac gcggcaaaa cggccgtggc 480
gaaggctcca aagctatttt catcaacacgc accaaccatc aaaaagtccg cgaagtggct 540
accggcaccg cccgcataat catcgacttc aatcctgcac accccgcgtg ggcttacgta 600
aaaaccgcaca cccggcagat tttcaaggta gatttgtatt cgatgcaggc ggtccgcagc 660
atcaagacag gttacaacgg ccccgccatg ggggtatccc gcgcacggcaa atacatcatg 720
gccggctct tcgtgccgc taacgcgtta atcctggatg ccgaaaccctt ggaaccgttg 780
aaaaccttcg aactggaaagg catcgatccc gacggtaaac atgtttcttc cgactcgggc 840
atgatcatcg gtacccctta tgcgcacgtt ttcgcgattt cgctggaaaa tgccggccag 900
gtctggatcg tcgattacaa caaagaaggc ttcccggtca cccaaatcga gaaagtggc 960
cgtcaactgc acgacgcctt cctgacgcatt ggcggcaaga aactgatggt ggcgtcttat 1020
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gcgggttgc tgccgcacgt cgggtggccgc gcggccggcgt tggttgcatt tcgtacctt 1140
ggcttcggtt ccaactttgg cgattgcac aagatggtcg tcagcgatgg ggatttgac 1200
aaaatggaaag tcgtcaaaca agtaccgggtt tcaggtggca ctgaatcgcc tgccggctcat 1260
gccaacgcac cttatgtcgc ggttgcacatc atcagcaaag acagacgtgc acgcaccatt 1320
cagttgatcg acaagaaaaac ccttggaaagg tccaaaactc tggatgtcgg cggccacgcc 1380
tacttccgg aatatagcgc cgacggcaaa ttccctctatg tcagtgccgg ctacaatggc 1440
gacgaagtgc tggtttacga ttccaaatacc ttgcaaaaag tggcgaccgt gccgatgaa 1500
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gacgaaatgg agcaaggcaa a 1581

<210> 60
<211> 527
<212> PRT
<213> *Methylomonas* 16a

<220>
<223> NorS

<400> 60

Met Met Lys Thr Thr Lys Arg Arg Leu Asn Gln Ser Leu Leu Ala
1 5 10 15

Ser Ala Ile Ala Ala Leu Leu Ser Ser Gly Ala Val Leu Ala Lys Ser
20 25 30

Asp Ser Pro His Asp Ile Tyr Met Asp Asn Cys Ala Ser Cys His Gly
 35 40 45

 Ala Asp His Gly Gly Tyr Leu Ala Pro Ala Leu Asn Ala Asp Thr Leu
 50 55 60

 Lys Gly Arg Ser Pro Thr Ala Leu Arg Thr Ile Val Met Ala Gly Ser
 65 70 75 80

 Phe Asp Thr Leu Met Pro Pro Phe Tyr Gly Lys Leu Ser Asp Asp Glu
 85 90 95

 Ile Arg Gly Val Ile Lys His Leu Gln Glu Thr Pro Lys Gln Pro Asn
 100 105 110

 Pro Ala Trp Thr Ile Asp Asp Met Lys Lys Ser Leu Lys Val Tyr Val
 115 120 125

 Lys Asp Glu Ser Thr Leu Pro Gly Lys Pro Thr Phe Gln Ile Asp Asn
 130 135 140

 Ile Asp Asn Leu Ile Gly Val Ala Ala Arg Gly Lys Tyr Gly Arg Gly
 145 150 155 160

 Glu Gly Ser Lys Ala Ile Phe Ile Asn Ser Thr Asn His Gln Lys Val
 165 170 175

 Gly Glu Val Ala Thr Gly Thr Ala Ala His Ile Ile Asp Phe Asn Pro
 180 185 190

 Ala Asn Pro Arg Trp Ala Tyr Val Lys Thr Asp Thr Ala Glu Ile Phe
 195 200 205

 Lys Val Asp Leu Tyr Ser Met Gln Ala Val Arg Ser Ile Lys Thr Gly
 210 215 220

 Tyr Asn Gly Pro Gly Met Gly Val Ser Arg Asp Gly Lys Tyr Ile Met
 225 230 235 240

 Ala Gly Ser Phe Val Pro His Asn Ala Val Ile Leu Asp Ala Glu Thr
 245 250 255

 Leu Glu Pro Leu Lys Thr Phe Glu Leu Glu Gly Ile Asp Pro Asp Gly
 260 265 270

 Lys His Val Ser Ser Asp Ser Gly Met Ile Ile Gly Thr Pro Tyr Ala
 275 280 285

 Asp Val Phe Ala Ile Ala Leu Glu Asn Ala Gly Gln Val Trp Ile Val
 290 295 300

 Asp Tyr Asn Lys Glu Gly Phe Pro Val Thr Lys Ile Glu Lys Val Gly
 305 310 315 320

 Arg His Leu His Asp Ala Phe Leu Thr His Gly Gly Lys Lys Leu Met
 325 330 335

 Val Ala Ser Tyr Asp Asp Ser Ile Val Ala Ala Ile Asp Leu Glu Lys
 340 345 350

Arg Glu Leu Ile Lys Gln Leu Pro Ala Gly Cys Val Pro His Val Gly
 355 360 365
 Gly Gly Ala Ala Val Val Val Asp Gly Arg Thr Leu Gly Phe Gly Thr
 370 375 380
 Asn Phe Gly Asp Cys Asp Lys Met Val Val Ser Val Trp Asp Leu Asp
 385 390 395 400
 Lys Met Glu Val Val Lys Gln Val Pro Val Ser Gly Gly Thr Glu Ser
 405 410 415
 Pro Ala Ala His Ala Asn Ala Pro Tyr Val Ala Val Asp Ile Ile Ser
 420 425 430
 Lys Asp Arg Arg Ala Arg Thr Ile Gln Leu Ile Asp Lys Lys Thr Leu
 435 440 445
 Glu Val Ala Lys Thr Leu Asp Val Gly Gly His Ala Tyr Phe Pro Glu
 450 455 460
 Tyr Ser Ala Asp Gly Lys Phe Leu Tyr Val Ser Ala Gly Tyr Asn Gly
 465 470 475 480
 Asp Glu Val Val Val Tyr Asp Ser Asn Thr Leu Gln Lys Val Ala Thr
 485 490 495
 Val Pro Met Glu Ser Pro Ala Gly Ile Phe Ser Arg Gly Arg Val Lys
 500 505 510
 Tyr Met Thr Arg Gly Leu Ser Pro Asp Glu Met Glu Gln Gly Lys
 515 520 525

Terpenoid genes

<210> 61
 <211> 1860
 <212> DNA
 <213> Methyloimonas 16a

<220>
 <223> DXS

<400> 61
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 gcgctgtcca aggaccagct ccagcaactg gctgacgagg tgccggccta tctgaccac 120
 acggtcagca ttcccgccgg ccattttgcg gccggcctcg gcaccgtgaa actgaccgtg 180
 gccttgcat t atgtgttcaa tacccccgtc gatcgttgg tctggacgt gggccatcg 240
 gcctatccgc acaagattct gaccggtcgc aaggagcgcg tgccgaccat tcgcacctg 300
 ggcggggtgt cagccttcc ggcgcgggac gagagcgaat acgtgcctt cggcgtcggc 360
 cattccagca cctcgatcag cgcggcactg ggcatggcca ttgcgtcgca gctgcgcggc 420
 gaagacaaga agatggtagc catcatcgcc gacggttcca tcaccggcgg catggcctat 480
 gagggcgtga atcatgccgg cgatgtgaat gccaacctgc tggatgttt gaaacgacaac 540
 gatatgtcga tctcgccgccc ggtcggggcg atgaacaatt atctgaccaa ggtgttgc 600
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 gtgtggaaac tggcgcccaa gaccgaggaa cacgtgaagg gcatgatcg tccccgttacc 720
 ttgttcgagg aattgggctt caattatttc ggcccgtatcg acggccatga tgcgagatg 780
 ctgggtcgaa ccctggaaaa tctgaaggat ttgaccgggc cggttccct gcatgtggtg 840
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ccggcttcg atccgaccaa ggatttcctg cccaaggcgg cgccgtcgcc gcacccgacc 960
 tataccgagg tggctggccg ctggctgtgc gacatggcgg ctcaagacga gcgcttgc 1020
 ggcacacgc cggcgatgcg cgaaggctct ggtttgggg aatttcaca gaaatttccg 1080
 aatcgctatt tcgatgtcgc catcgccgag cagcatgcgg tgaccttgc cgccggccag 1140
 gcctgccagg gcgccaagcc ggtggtggcg atttattcca ccttcctgca acgcggttac 1200
 gatcagttga tccacgacgt ggccttgcag aacttagata tgctttgc actggatcg 1260
 gccggcttgg tcggccccga tggaccgacc catgctggcg cctttgatta cagctacatg 1320
 cgctgtattc cgaacatgct gatcatggct ccagccgacg agaacgagtg caggcagatg 1380
 ctgaccacccg gcttccaaca ccatggcccg gcttcgggtgc gctatcccg cgccaaagg 1440
 cccggggccgg caatcgatcc gaccctgacc ggcgtggaga tcggcaaggc cgaagtca 1500
 caccacggca gcccgcacgc cattctggcc tggggcagca tggtcacgccc tgccgtcgaa 1560
 gccggcaagc agctgggcgc gacgggtggtg aacatgcgt tcgtcaagcc gttcgatcaa 1620
 gccttgggtgc tggaaatttggc caggacgcac gatgtgttcg tcaccgtcga gaaaaacg 1680
 atcgccggcg ggcgtggcag tgcgatcaac accttcctgc aggccagaa ggtgctgatg 1740
 ccggtctgca acatcgccct gcccgaccgc ttctcgagc aaggtagtcg cgaggaattt 1800
 ctcagcctgg tcggcctcga cagcaagggc atcctcgcca ccatcgaaaca gttttgcgct 1860

<210> 62

<211> 620

<212> PRT

<213> Methylomonas 16a

<220>

<223> Amino acid sequences encoded by DXS

<400> 62

Met	Lys	Leu	Thr	Thr	Asp	Tyr	Pro	Leu	Leu	Lys	Asn	Ile	His	Thr	Pro
1								5		10				15	

Ala	Asp	Ile	Arg	Ala	Leu	Ser	Lys	Asp	Gln	Leu	Gln	Gln	Leu	Ala	Asp
										20		25		30	

Glu	Val	Arg	Gly	Tyr	Leu	Thr	His	Thr	Val	Ser	Ile	Ser	Gly	Gly	His
										35		40		45	

Phe	Ala	Ala	Gly	Leu	Gly	Thr	Val	Glu	Leu	Thr	Val	Ala	Leu	His	Tyr
								50		55		60			

Val	Phe	Asn	Thr	Pro	Val	Asp	Gln	Leu	Val	Trp	Asp	Val	Gly	His	Gln
								65		70		75		80	

Ala	Tyr	Pro	His	Lys	Ile	Leu	Thr	Gly	Arg	Lys	Glu	Arg	Met	Pro	Thr
								85		90		95			

Ile	Arg	Thr	Leu	Gly	Gly	Val	Ser	Ala	Phe	Pro	Ala	Arg	Asp	Glu	Ser
								100		105		110			

Glu	Tyr	Asp	Ala	Phe	Gly	Val	Gly	His	Ser	Ser	Thr	Ser	Ile	Ser	Ala
								115		120		125			

Ala	Leu	Gly	Met	ala	Ile	Ala	Ser	Gln	Leu	Arg	Gly	Glu	Asp	Lys	Lys
								130		135		140			

Met	Val	Ala	Ile	Ile	Gly	Asp	Gly	Ser	Ile	Thr	Gly	Gly	Met	ala	Tyr
								145		150		155		160	

Glu	Ala	Met	Asn	His	Ala	Gly	Asp	Val	Asn	Ala	Asn	Leu	Leu	Val	Ile
								165		170		175			

Leu Asn Asp Asn Asp Met Ser Ile Ser Pro Pro Val Gly Ala Met Asn
 180 185 190
 Asn Tyr Leu Thr Lys Val Leu Ser Ser Lys Phe Tyr Ser Ser Val Arg
 195 200 205
 Glu Glu Ser Lys Lys Ala Leu Ala Lys Met Pro Ser Val Trp Glu Leu
 210 215 220
 Ala Arg Lys Thr Glu Glu His Val Lys Gly Met Ile Val Pro Gly Thr
 225 230 235 240
 Leu Phe Glu Glu Leu Gly Phe Asn Tyr Phe Gly Pro Ile Asp Gly His
 245 250 255
 Asp Val Glu Met Leu Val Ser Thr Leu Glu Asn Leu Lys Asp Leu Thr
 260 265 270
 Gly Pro Val Phe Leu His Val Val Thr Lys Lys Gly Lys Gly Tyr Ala
 275 280 285
 Pro Ala Glu Lys Asp Pro Leu Ala Tyr His Gly Val Pro Ala Phe Asp
 290 295 300
 Pro Thr Lys Asp Phe Leu Pro Lys Ala Ala Pro Ser Pro His Pro Thr
 305 310 315 320
 Tyr Thr Glu Val Phe Gly Arg Trp Leu Cys Asp Met Ala Ala Gln Asp
 325 330 335
 Glu Arg Leu Leu Gly Ile Thr Pro Ala Met Arg Glu Gly Ser Gly Leu
 340 345 350
 Val Glu Phe Ser Gln Lys Phe Pro Asn Arg Tyr Phe Asp Val Ala Ile
 355 360 365
 Ala Glu Gln His Ala Val Thr Leu Ala Ala Gly Gln Ala Cys Gln Gly
 370 375 380
 Ala Lys Pro Val Val Ala Ile Tyr Ser Thr Phe Leu Gln Arg Gly Tyr
 385 390 395 400
 Asp Gln Leu Ile His Asp Val Ala Leu Gln Asn Leu Asp Met Leu Phe
 405 410 415
 Ala Leu Asp Arg Ala Gly Leu Val Gly Pro Asp Gly Pro Thr His Ala
 420 425 430
 Gly Ala Phe Asp Tyr Ser Tyr Met Arg Cys Ile Pro Asn Met Leu Ile
 435 440 445
 Met Ala Pro Ala Asp Glu Asn Glu Cys Arg Gln Met Leu Thr Thr Gly
 450 455 460
 Phe Gln His His Gly Pro Ala Ser Val Arg Tyr Pro Arg Gly Lys Gly
 465 470 475 480
 Pro Gly Ala Ala Ile Asp Pro Thr Leu Thr Ala Leu Glu Ile Gly Lys
 485 490 495

Ala Glu Val Arg His His Gly Ser Arg Ile Ala Ile Leu Ala Trp Gly
500 505 510

Ser Met Val Thr Pro Ala Val Glu Ala Gly Lys Gln Leu Gly Ala Thr
515 520 525

Val Val Asn Met Arg Phe Val Lys Pro Phe Asp Gln Ala Leu Val Leu
530 535 540

Glu Leu Ala Arg Thr His Asp Val Phe Val Thr Val Glu Glu Asn Val
545 550 555 560

Ile Ala Gly Gly Ala Gly Ser Ala Ile Asn Thr Phe Leu Gln Ala Gln
565 570 575

Lys Val Leu Met Pro Val Cys Asn Ile Gly Leu Pro Asp Arg Phe Val
580 585 590

Glu Gln Gly Ser Arg Glu Glu Leu Leu Ser Leu Val Gly Leu Asp Ser
595 600 605

Lys Gly Ile Leu Ala Thr Ile Glu Gln Phe Cys Ala
610 615 620

<210> 63

<211> 1182

<212> DNA

<213> Methylomonas 16a

<220>

<223> DXR

<400> 63

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gcattgtatg aacaatgcct ggcccaccat ccggagatatg cgggtgttgt catggaaagc 180
aaggtagcag agtcaaaca gcgcattgcc gcttcgcccc tagcggatat caaggtttg 240
tcgggtagcg aggcccttgca acagggtggcc acgctggaaa acgtcgatac ggtgatggcg 300
gctatcgctg gcgcggccgg attgttgcgg accttggccg cggccaaggc cggcaaaacc 360
gtgctgttgtt ccaacaagga agccttgggt atgtcgggac aaatcttcat gcaggccgtc 420
agcgattccg gcgcgtgttt gctgccata gacagcgagc acaacgcccattttcagtgc 480
atgcccggcg gttatacgcc aggccataca gccaaacagg cgcccgcattttattgacc 540
gcttccgggtg gcccatttcg acggacgccc atagaaacgt tgcgcgcgt cacgcggat 600
caggccgtt cccatcctaa atgggacatg gggcgcaaga ttccggcgtca ttccgcacc 660
atgatgaaca aaggtctcga actgatcgaa gcctgcttgt tttcaacat ggagcccac 720
cagattgaag tcgtcattca tccgcagagc atcatttcatt cgatgggttgcatgtcgat 780
ggttcggtt tggcgcagat gggtaatccc gacatgcgcg cggcgatagc gcacgcgt 840
gcctggccgg aacgcttga ctctgggtgt ggcgcgtgg atatttcga agtagggcac 900
atggatttcg aaaaacccga cttgaaacgg ttcccttgc tgagattggc ttatgaagcc 960
atcaagtcg gtgaaattat gccaacggta ttgaacgcag ccaatgaaat tgctgtcgaa 1020
gcgttttaa atgaagaagt caaatttact gacatgcgg tcatcatcga ggcgcagcatg 1080
gcccagttt aaccggacga tgccggcagc ctcgaattgg ttttgcaggc cgatcaagat 1140
gcgcgcgagg tggcttagaga catcatcaag accttggtag ct 1182

<210> 64

<211> 394

<212> PRT

<213> Methylomonas 16a

<220>

<223> Amino acid sequences encoded by DXR

<400> 64

Met Lys Gly Ile Cys Ile Leu Gly Ala Thr Gly Ser Ile Gly Val Ser
1 5 10 15

Thr Leu Asp Val Val Ala Arg His Pro Asp Lys Tyr Gln Val Val Ala
20 25 30

Leu Thr Ala Asn Gly Asn Ile Asp Ala Leu Tyr Glu Gln Cys Leu Ala
35 40 45

His His Pro Glu Tyr Ala Val Val Val Met Glu Ser Lys Val Ala Glu
50 55 60

Phe Lys Gln Arg Ile Ala Ala Ser Pro Val Ala Asp Ile Lys Val Leu
65 70 75 80

Ser Gly Ser Glu Ala Leu Gln Gln Val Ala Thr Leu Glu Asn Val Asp
85 90 95

Thr Val Met Ala Ala Ile Val Gly Ala Ala Gly Leu Leu Pro Thr Leu
100 105 110

Ala Ala Ala Lys Ala Gly Lys Thr Val Leu Leu Ala Asn Lys Glu Ala
115 120 125

Leu Val Met Ser Gly Gln Ile Phe Met Gln Ala Val Ser Asp Ser Gly
130 135 140

Ala Val Leu Leu Pro Ile Asp Ser Glu His Asn Ala Ile Phe Gln Cys
145 150 155 160

Met Pro Ala Gly Tyr Thr Pro Gly His Thr Ala Lys Gln Ala Arg Arg
165 170 175

Ile Leu Leu Thr Ala Ser Gly Gly Pro Phe Arg Arg Thr Pro Ile Glu
180 185 190

Thr Leu Ser Ser Val Thr Pro Asp Gln Ala Val Ala His Pro Lys Trp
195 200 205

Asp Met Gly Arg Lys Ile Ser Val Asp Ser Ala Thr Met Met Asn Lys
210 215 220

Gly Leu Glu Leu Ile Glu Ala Cys Leu Leu Phe Asn Met Glu Pro Asp
225 230 235 240

Gln Ile Glu Val Val Ile His Pro Gln Ser Ile Ile His Ser Met Val
245 250 255

Asp Tyr Val Asp Gly Ser Val Leu Ala Gln Met Gly Asn Pro Asp Met
260 265 270

Arg Thr Pro Ile Ala His Ala Met Ala Trp Pro Glu Arg Phe Asp Ser
275 280 285

Gly Val Ala Pro Leu Asp Ile Phe Glu Val Gly His Met Asp Phe Glu
290 295 300

Lys	Pro	Asp	Leu	Lys	Arg	Phe	Pro	Cys	Leu	Arg	Leu	Ala	Tyr	Glu	Ala
305															320
Ile	Lys	Ser	Gly	Gly	Ile	Met	Pro	Thr	Val	Leu	Asn	Ala	Ala	Asn	Glu
			325						330						335
Ile	Ala	Val	Glu	Ala	Phe	Leu	Asn	Glu	Glu	Val	Lys	Phe	Thr	Asp	Ile
		340						345							350
Ala	Val	Ile	Ile	Glu	Arg	Ser	Met	ala	Gln	Phe	Lys	Pro	Asp	Asp	Ala
			355					360							365
Gly	Ser	Leu	Glu	Leu	Val	Leu	Gln	Ala	Asp	Gln	Asp	Ala	Arg	Glu	Val
			370				375								380
Ala	Arg	Asp	Ile	Ile	Lys	Thr	Leu	Val	Ala						
			385				390								

<210> 65
<211> 471
<212> DNA
<213> Methyloimonas 16a

<220>
<223> ISPF

<400> 65
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gtgtgcacg cattggccga cgccatcttggagccgcgg ctttgggcga catcgccaaa 180
catttcccgacacc caatttcaag ggccgcgaca gcagggtgt actgcgcac 240
gtgtacggca tcgtcaagga aaaaggcttat aaactgttca acgccgacgt gaccatcatc 300
gctcaggcgccga cgaagatgct gcccacacgtg cccggcatgc ggcacaacat tgccgcogat 360
ctggaaacctgatgtt cattaatgtaaagccacga cgaccgagaa actgggcttt 420
gagggccgta aggaaggcat cgccgtgcag gctgtggtgt tgatagaacg c 471

<210> 66
<211> 157
<212> PRT
<213> Methyloimonas 16a

<220>
<223> Amino acid sequences encoded by ISPF
<400> 66
Met Ile Arg Val Gly Met Gly Tyr Asp Val His Arg Phe Asn Asp Gly
1 5 10 15

Asp His Ile Ile Leu Gly Gly Val Lys Ile Pro Tyr Glu Lys Gly Leu
20 25 30

Glu Ala His Ser Asp Gly Asp Val Val Leu His Ala Leu Ala Asp Ala
35 40 45

Ile Leu Gly Ala Ala Ala Leu Gly Asp Ile Gly Lys His Phe Pro Asp
50 55 60

Thr Asp Pro Asn Phe Lys Gly Ala Asp Ser Arg Val Leu Leu Arg His
65 70 75 80

Val Tyr Gly Ile Val Lys Glu Lys Gly Tyr Lys Leu Val Asn Ala Asp
85 90 95

Val Thr Ile Ile Ala Gln Ala Pro Lys Met Leu Pro His Val Pro Gly
100 105 110

Met Arg Ala Asn Ile Ala Ala Asp Leu Glu Thr Asp Val Asp Phe Ile
115 120 125

Asn Val Lys Ala Thr Thr Glu Lys Leu Gly Phe Glu Gly Arg Lys
130 135 140

Glu Gly Ile Ala Val Gln Ala Val Val Leu Ile Glu Arg
145 150 155

<210> 67

<211> 693

<212> DNA

<213> Methylomonas 16a

<220>

<223> ISPD

<400> 67

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caagccgatc gccccaaaca atatttacccg cttgccggta aaacggtcat cgaacacaca 120
ctgactcgac tacttgagtc cgacgccttc caaaaagtgg cggtggcgat ttccgtcgaa 180
gacccttatt ggccctgaact gtccatagcc aaacaccccg acatcatcac cgccgcctggc 240
ggcaaggaac gcggccgactc ggtgctgtct gcactgaagg cttagaaga tatagccagc 300
gaaaatgatt gggtgctggt acacgacgcc gccccccct gcttgacggg cagcgacatc 360
caccttcaaa tcgatacctt aaaaaatgac cccgtcgccg gcatccctggc cttgagttcg 420
cacgacacat tgaaacacgt ggatggtgac acgatcaccc caaccataga cagaaagcac 480
gtctggcgcg cttgacgcc gcaaattttc aaatacggca tggcgcgca cgcgttgcaa 540
cgAACCGAAG gcaatccggc cgtaaccggac gaagccagtgcgctggact tttggccat 600
aaACCCAAAAA tcgtggagg ccgccccggac aacatcaaaa tcacccggccc ggaagatttg 660
gccctggcac aattttatat ggagcaacaa gca 693

<210> 68

<211> 231

<212> PRT

<213> Methylomonas 16a

<220>

<223> Amino acid sequences encoded by ISPD

<400> 68

Met Asn Pro Thr Ile Gln Cys Trp Ala Val Val Pro Ala Ala Gly Val
1 5 10 15

Gly Lys Arg Met Gln Ala Asp Arg Pro Lys Gln Tyr Leu Pro Leu Ala
20 25 30

Gly Lys Thr Val Ile Glu His Thr Leu Thr Arg Leu Leu Glu Ser Asp
35 40 45

Ala Phe Gln Lys Val Ala Val Ala Ile Ser Val Glu Asp Pro Tyr Trp
 50 55 60

Pro Glu Leu Ser Ile Ala Lys His Pro Asp Ile Ile Thr Ala Pro Gly
 65 70 75 80

Gly Lys Glu Arg Ala Asp Ser Val Leu Ser Ala Leu Lys Ala Leu Glu
 85 90 95

Asp Ile Ala Ser Glu Asn Asp Trp Val Leu Val His Asp Ala Ala Arg
 100 105 110

Pro Cys Leu Thr Gly Ser Asp Ile His Leu Gln Ile Asp Thr Leu Lys
 115 120 125

Asn Asp Pro Val Gly Gly Ile Leu Ala Leu Ser Ser His Asp Thr Leu
 130 135 140

Lys His Val Asp Gly Asp Thr Ile Thr Ala Thr Ile Asp Arg Lys His
 145 150 155 160

Val Trp Arg Ala Leu Thr Pro Gln Met Phe Lys Tyr Gly Met Leu Arg
 165 170 175

Asp Ala Leu Gln Arg Thr Glu Gly Asn Pro Ala Val Thr Asp Glu Ala
 180 185 190

Ser Ala Leu Glu Leu Leu Gly His Lys Pro Lys Ile Val Glu Gly Arg
 195 200 205

Pro Asp Asn Ile Lys Ile Thr Arg Pro Glu Asp Leu Ala Leu Ala Gln
 210 215 220

Phe Tyr Met Glu Gln Gln Ala
 225 230

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210> 69  
<211> 1632  
<212> DNA  
<213> Methylomonas 16a
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<220>
<223> PYRG

<400> 69

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gtgaccgaag	acggtgccg	aaccgattt	gaccttggcc	attacgaacg	gttttgaaa	240
accacgatga	ccaagaaaaa	caacttcacc	accggtcagg	tttacgagca	ggtattacgc	300
aacgagcgca	aaggtgatta	tcttggcgcg	accgtgcaag	tcattccaca	tatcaccgcac	360
gaaatcaaac	gccgggtgta	tgaaagcgcc	gaagggaaaag	atgtggcatt	gatcgaagtc	420
ggcggcacgg	tggcgacat	cgaatcgta	ccgttctgg	aaaccatacg	ccagatggc	480
gtggaaactgg	gtcgtgaccg	cgcctgttc	attcatttga	cgctgggtcc	ttacatcaa	540
tcggccggcg	aactgaaaac	caagcccacc	cagcatttgg	tcaaagaact	gcgcaccatc	600
gggattcagc	cgacatttt	gatctgttgt	tcagaacaac	cgatcccgcc	cagtgaacgc	660
cgcaagatcg	cgctatttac	caatgtcgcc	gaaaaggcgg	tgatttccgc	gatcgatgcc	720
gacaccattt	accgattcc	gctattgtcg	cgcgaacaag	gcctggacga	cctgggtgtc	780
gatcaggatgc	gcctggacgt	accagcggcg	gatttatcg	cctggggaaaa	ggtcgtcgat	840

ggcctgactc atccgaccga cgaagtcagc attgcgatcg tcggtaata tgcgaccac 900
 accgatgcct acaaatcgct gaatgaagcc ctgattcatg ccggcattca cacgcgccac 960
 aagggtcaaa tcagctacat cgactccgaa accatagaag ccgaaggcac cgccaaattg 1020
 aaaaacgtcg atgcgatcct ggtgccgggt gtttcgccg aacgcggcgt ggaaggcaag 1080
 atttctaccg tgcgtttgc ccgcgagaac aaaatcccgt atttggcat ttgcttggc 1140
 atgcaatcg cggtaatcga attcgcccgc aacgtggttg gccttggagg cgcgacacgc 1200
 accgaattcc tgccgaaatc gccacaccct gtgatcggt tgatcaccga atggatggac 1260
 gaagccggcg aactggtcac acgcgacgaa gattccgatc tggccggcac gatgcgtctg 1320
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 gtcatcaccg agcgtcaccg ccaccgctac gaattcaaca atcaatattt aaaacaactg 1440
 gaagcggccg gcatgaaatt ttccggtaaa tcgctggacg gcccctgggt ggagatcatc 1500
 gagctacccg aacacccctg gttcctggcc tgccagttcc atccgaatt cacctcgacg 1560
 ccgcgttaacg gccacgcctt atttcgggc ttcaaggat cggccgccaa acacaaaaca 1620
 caaggcacag ca 1632

<210> 70

<211> 544

<212> PRT

<213> Methylomonas 16a

<220>

<223> Amino acid sequences encoded by ORF6 - PYRG

<400> 70

Met Thr Lys Phe Ile Phe Ile Thr Gly Gly Val Val Ser Ser Leu Gly
 1 5 10 15

Lys Gly Ile Ala Ala Ser Ser Leu Ala Ala Ile Leu Glu Asp Arg Gly
 20 25 30

Leu Lys Val Thr Ile Thr Lys Leu Asp Pro Tyr Ile Asn Val Asp Pro
 35 40 45

Gly Thr Met Ser Pro Phe Gln His Gly Glu Val Phe Val Thr Glu Asp
 50 55 60

Gly Ala Glu Thr Asp Leu Asp Leu Gly His Tyr Glu Arg Phe Leu Lys
 65 70 75 80

Thr Thr Met Thr Lys Lys Asn Asn Phe Thr Thr Gly Gln Val Tyr Glu
 85 90 95

Gln Val Leu Arg Asn Glu Arg Lys Gly Asp Tyr Leu Gly Ala Thr Val
 100 105 110

Gln Val Ile Pro His Ile Thr Asp Glu Ile Lys Arg Arg Val Tyr Glu
 115 120 125

Ser Ala Glu Gly Lys Asp Val Ala Leu Ile Glu Val Gly Thr Val
 130 135 140

Gly Asp Ile Glu Ser Leu Pro Phe Leu Glu Thr Ile Arg Gln Met Gly
 145 150 155 160

Val Glu Leu Gly Arg Asp Arg Ala Leu Phe Ile His Leu Thr Leu Val
 165 170 175

Pro Tyr Ile Lys Ser Ala Gly Glu Leu Lys Thr Lys Pro Thr Gln His
 180 185 190

Ser Val Lys Glu Leu Arg Thr Ile Gly Ile Gln Pro Asp Ile Leu Ile
 195 200 205
 Cys Arg Ser Glu Gln Pro Ile Pro Ala Ser Glu Arg Arg Lys Ile Ala
 210 215 220
 Leu Phe Thr Asn Val Ala Glu Lys Ala Val Ile Ser Ala Ile Asp Ala
 225 230 235 240
 Asp Thr Ile Tyr Arg Ile Pro Leu Leu Arg Glu Gln Gly Leu Asp
 245 250 255
 Asp Leu Val Val Asp Gln Leu Arg Leu Asp Val Pro Ala Ala Asp Leu
 260 265 270
 Ser Ala Trp Glu Lys Val Val Asp Gly Leu Thr His Pro Thr Asp Glu
 275 280 285
 Val Ser Ile Ala Ile Val Gly Lys Tyr Val Asp His Thr Asp Ala Tyr
 290 295 300
 Lys Ser Leu Asn Glu Ala Leu Ile His Ala Gly Ile His Thr Arg His
 305 310 315 320
 Lys Val Gln Ile Ser Tyr Ile Asp Ser Glu Thr Ile Glu Ala Glu Gly
 325 330 335
 Thr Ala Lys Leu Lys Asn Val Asp Ala Ile Leu Val Pro Gly Gly Phe
 340 345 350
 Gly Glu Arg Gly Val Glu Gly Lys Ile Ser Thr Val Arg Phe Ala Arg
 355 360 365
 Glu Asn Lys Ile Pro Tyr Leu Gly Ile Cys Leu Gly Met Gln Ser Ala
 370 375 380
 Val Ile Glu Phe Ala Arg Asn Val Val Gly Leu Glu Gly Ala His Ser
 385 390 395 400
 Thr Glu Phe Leu Pro Lys Ser Pro His Pro Val Ile Gly Leu Ile Thr
 405 410 415
 Glu Trp Met Asp Glu Ala Gly Glu Leu Val Thr Arg Asp Glu Asp Ser
 420 425 430
 Asp Leu Gly Gly Thr Met Arg Leu Gly Ala Gln Lys Cys Arg Leu Lys
 435 440 445
 Ala Asp Ser Leu Ala Phe Gln Leu Tyr Gln Lys Asp Val Ile Thr Glu
 450 455 460
 Arg His Arg His Arg Tyr Glu Phe Asn Asn Gln Tyr Leu Lys Gln Leu
 465 470 475 480
 Glu Ala Ala Gly Met Lys Phe Ser Gly Lys Ser Leu Asp Gly Arg Leu
 485 490 495
 Val Glu Ile Ile Glu Leu Pro Glu His Pro Trp Phe Leu Ala Cys Gln
 500 505 510

Phe His Pro Glu Phe Thr Ser Thr Pro Arg Asn Gly His Ala Leu Phe
515 520 525

Ser Gly Phe Val Glu Ala Ala Ala Lys His Lys Thr Gln Gly Thr Ala
530 535 540

<210> 71
<211> 891
<212> DNA
<213> Methyloimonas 16a

<220>
<223> ORF7 ISPA
<400> 71

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gcccgtctgc ctgcccggaaa catactgcca caaaccttgc atcaggccat ggcgtattcc 120
gtattgaacg gcggcaaacg caccggcccc ttgttgactt atgcgaccgg tcaggctttg 180
ggcttgcggg aaaaacgtgct ggatgcggcg gcttgcgcgg tagaattcat ccatgtgtat 240
tcgctgattc acgacgatct gccggccatg gacaacgatg atctgcgcgg cggcaaacccg 300
acctgtcaca aggcttacga cgaggccacc gccatttgg ccggcgacgc actgcaggcg 360
ctggccttg aagttctggc caacgacccc ggcacatcaccc tcgatgcaccc ggctcgccctg 420
aaaatgatca cggcttgcac ccgcgcgcggc ggctctcaag gcatgggtggg cggtaagcc 480
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cacaagactg gcgcgcgtat ccgcgcgcggc gtcaatctgg cggcattatc caaaccggat 600
ctggataactt gcgtcgccaa gaaactggat cactatgcacca aatgcataagg cttgtcggttc 660
caggtcaaaag acgacattct cgacatcgaa gcccggacccg cgacactcgg caagactcag 720
ggcaaggaca tgcataaacga caaaccggacc taccctgcgc tattgggcat ggctggcgcc 780
aaacaaaaaaag cccaggaatt gcacgaacaa gcagtcgaaa gcttaacggg atttggcagc 840
gaagccgacc tgctgcgcga actatcgctt tacatcatcg agcgcacgc 891

<210> 72
<211> 297
<212> PRT
<213> Methyloimonas 16a

<220>

<223> Amino acid sequences encoded by ORF7 - ISPA

<400> 72

Met Ser Lys Leu Lys Ala Tyr Leu Thr Val Cys Gln Glu Arg Val Glu
1 5 10 15

Arg Ala Leu Asp Ala Arg Leu Pro Ala Glu Asn Ile Leu Pro Gln Thr
20 25 30

Leu His Gln Ala Met Arg Tyr Ser Val Leu Asn Gly Gly Lys Arg Thr
35 40 45

Arg Pro Leu Leu Thr Tyr Ala Thr Gly Gln Ala Leu Gly Leu Pro Glu
50 55 60

Asn Val Leu Asp Ala Pro Ala Cys Ala Val Glu Phe Ile His Val Tyr
65 70 75 80

Ser Leu Ile His Asp Asp Leu Pro Ala Met Asp Asn Asp Asp Leu Arg
85 90 95

Arg Gly Lys Pro Thr Cys His Lys Ala Tyr Asp Glu Ala Thr Ala Ile
100 105 110

Leu Ala Gly Asp Ala Leu Gln Ala Leu Ala Phe Glu Val Leu Ala Asn
 115 120 125
 Asp Pro Gly Ile Thr Val Asp Ala Pro Ala Arg Leu Lys Met Ile Thr
 130 135 140
 Ala Leu Thr Arg Ala Ser Gly Ser Gln Gly Met Val Gly Gly Gln Ala
 145 150 155 160
 Ile Asp Leu Gly Ser Val Gly Arg Lys Leu Thr Leu Pro Glu Leu Glu
 165 170 175
 Asn Met His Ile His Lys Thr Gly Ala Leu Ile Arg Ala Ser Val Asn
 180 185 190
 Leu Ala Ala Leu Ser Lys Pro Asp Leu Asp Thr Cys Val Ala Lys Lys
 195 200 205
 Leu Asp His Tyr Ala Lys Cys Ile Gly Leu Ser Phe Gln Val Lys Asp
 210 215 220
 Asp Ile Leu Asp Ile Glu Ala Asp Thr Ala Thr Leu Gly Lys Thr Gln
 225 230 235 240
 Gly Lys Asp Ile Asp Asn Asp Lys Pro Thr Tyr Pro Ala Leu Leu Gly
 245 250 255
 Met Ala Gly Ala Lys Gln Lys Ala Gln Glu Leu His Glu Gln Ala Val
 260 265 270
 Glu Ser Leu Thr Gly Phe Gly Ser Glu Ala Asp Leu Leu Arg Glu Leu
 275 280 285
 Ser Leu Tyr Ile Ile Glu Arg Thr His
 290 295

<210> 73
 <211> 855
 <212> DNA
 <213> Methyloimonas 16a

<220>
 <223> ISPE
 <400> 73
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 ctcgatctat gcgttgcgtt gacgttccat ccgttgcgt atggccgcgt gacgctgcga 180
 aatccaaatct ccggcggttcc agagcaggat gacttgactg ttcggccgc taatttgg 240
 aagtctcata ccggctgtgt ggcggagtt tgtatcgata tcgagaaaaa tctgcctatg 300
 ggtgggtgtt tgggtgggtgg aagttccat gctgctacaa cttgggtgt tctaaatcg 360
 ctttggggct tgggtttgtc gaagcgttag ttgatggatt tgggtttgtc gcttgggtgcc 420
 gatgtgcctg tggttgcgtt tggttgcgt gcctggggcg aagggtgttag cgaggatgg 480
 caggcaataa cgttgccgga acaatggttt gtcatcattt aaccggattt ccatgtgaat 540
 actggagaaa tttttctgc agaaaattt acaaggaata gtgcagtcgt tacaatgagc 600
 gactttcttgc cagggataa tcgaaatgtat tggttcggaaag tggttgcgtt gttatatcg 660
 ccgggtgaag atgcaatcgat tgcgttgcgtt tgctatgcgg aagcgagatt gacggggacc 720
 ggtgcgttgc tggttgcgtt aaggaaatgtat ctgagatgtgc gtttgcgtt 780

ttgaaaagatc ggtggctggc gttcttggct aaaggcttga atcagtctgc gctctacaag 840
aaatttagaac aggaa 855

<210> 74
<211> 285
<212> PRT
<213> Methylomonas 16a

<220>
<223> Amino acid sequences encoded by ISPE

<400> 74
Met Asp Tyr Ala Ala Gly Trp Gly Glu Arg Trp Pro Ala Pro Ala Lys
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Leu Asn Leu Met Leu Arg Ile Thr Gly Arg Arg Pro Asp Gly Tyr His
20 25 30

Leu Leu Gln Thr Val Phe Gln Met Leu Asp Leu Cys Asp Trp Leu Thr
35 40 45

Phe His Pro Val Asp Asp Gly Arg Val Thr Leu Arg Asn Pro Ile Ser
50 55 60

Gly Val Pro Glu Gln Asp Asp Leu Thr Val Arg Ala Ala Asn Leu Leu
65 70 75 80

Lys Ser His Thr Gly Cys Val Arg Gly Val Cys Ile Asp Ile Glu Lys
85 90 95

Asn Leu Pro Met Gly Gly Leu Gly Gly Ser Ser Asp Ala Ala
100 105 110

Thr Thr Leu Val Val Leu Asn Arg Leu Trp Gly Leu Gly Leu Ser Lys
115 120 125

Arg Glu Leu Met Asp Leu Gly Leu Arg Leu Gly Ala Asp Val Pro Val
130 135 140

Phe Val Phe Gly Cys Ser Ala Trp Gly Glu Gly Val Ser Glu Asp Leu
145 150 155 160

Gln Ala Ile Thr Leu Pro Glu Gln Trp Phe Val Ile Ile Lys Pro Asp
165 170 175

Cys His Val Asn Thr Gly Glu Ile Phe Ser Ala Glu Asn Leu Thr Arg
180 185 190

Asn Ser Ala Val Val Thr Met Ser Asp Phe Leu Ala Gly Asp Asn Arg
195 200 205

Asn Asp Cys Ser Glu Val Val Cys Lys Leu Tyr Arg Pro Val Lys Asp
210 215 220

Ala Ile Asp Ala Leu Leu Cys Tyr Ala Glu Ala Arg Leu Thr Gly Thr
225 230 235 240

Gly Ala Cys Val Phe Ala Gln Phe Cys Asn Lys Glu Asp Ala Glu Ser
245 250 255

Ala Leu Glu Gly Leu Lys Asp Arg Trp Leu Val Phe Leu Ala Lys Gly
260 265 270

Leu Asn Gln Ser Ala Leu Tyr Lys Lys Leu Glu Gln Gly
275 280 285

<210> 75
<211> 1533
<212> DNA
<213> Methylomonas 16a

<220>
<223> CRTN1

<400> 75
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ggccgcacc gcccgcataa catgaacggc ttacccctcg ataccggtcc gacattttg 180
ttgatgaaag gcgtgcttgcg cggaaatgttc gaactgtgcg agcggccgtag cgaggattat 240
ctggaaattcc tggcgctaag cccgatgtac cgccctgtgt acgacgaccg cgacatctc 300
gtctattccg accgcgagaa catgcgcgcg gaatttgcac gggtattcga cgaaggcacg 360
gacggctacg aacagtccat ggaacaggaa cgccaaacgct tcaacgcgcgt gtatccctgc 420
atcaccccgq attattccag cctgaaaatcc tttttgtcgc tggacttgat caaggccctg 480
ccgtggctgg cttttccgaa aagcgtgttc aataatctcg gccagtttta caaccaggaa 540
aaaatgcgcc tggcccttttgc ctttcagttcc aagtatctgg gcatgtcgcc gtggaaatgc 600
ccggcactgt ttacgatgtc gcccatactg gagcacgaat acggcattta tcacgtcaaa 660
ggcggcctga accgcatcgc ggcggcgatg ggcgaagtga tcgccccaaaa cggcggcgaa 720
attcacttga acagcgaat ctagtcgtatc atcatcgaaa acggcgtgc caagggcgtc 780
aaattacaac atggcgcggc gctgcgcggc gacgaagtca tcataacgc ggattttgcc 840
cacgcgtatga cgcatactggt caaacccggc gtcttgcac aatacaccggc ggaaaacctg 900
aaggcagcgcg agtattccgt ttcgacccatc atgctgtatc tgggtttggc caagattac 960
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atcacgcgcg aaacctgggaa aacggacgaa cacgttaca agggcgccac tttcagtttg 1320
tcgcacaagt tcagccaaat gctgtactgg cggccgcaca accgtttcga ggaactgccc 1380
aattgtatc tggcgccgg cggcacgat cccggtagcg gtttgcgcac catctacgaa 1440
tcggcgccgg tttcgccaa gctgatttcc cagaaacatc gggtgagggtt caaggacata 1500
gcacacagcg cctggctgaa aaaagccaaa gcc 1533

<210> 76
<211> 511
<212> PRT
<213> Methylomonas 16a

<220>
<223> Amino acid sequences encoded by CRTN1
<400> 76

Met ala Asn Thr Lys His Ile Ile Ile Val Gly Ala Gly Pro Gly Gly
1 5 10 15

Leu Cys Ala Gly Met Leu Leu Ser Gln Arg Gly Phe Lys Val Ser Ile
20 25 30

Phe Asp Lys His Ala Glu Ile Gly Gly Arg Asn Arg Pro Ile Asn Met
 35 40 45

 Asn Gly Phe Thr Phe Asp Thr Gly Pro Thr Phe Leu Leu Met Lys Gly
 50 55 60

 Val Leu Asp Glu Met Phe Glu Leu Cys Glu Arg Arg Ser Glu Asp Tyr
 65 70 75 80

 Leu Glu Phe Leu Pro Leu Ser Pro Met Tyr Arg Leu Leu Tyr Asp Asp
 85 90 95

 Arg Asp Ile Phe Val Tyr Ser Asp Arg Glu Asn Met Arg Ala Glu Leu
 100 105 110

 Gln Arg Val Phe Asp Glu Gly Thr Asp Gly Tyr Glu Gln Phe Met Glu
 115 120 125

 Gln Glu Arg Lys Arg Phe Asn Ala Leu Tyr Pro Cys Ile Thr Arg Asp
 130 135 140

 Tyr Ser Ser Leu Lys Ser Phe Leu Ser Leu Asp Leu Ile Lys Ala Leu
 145 150 155 160

 Pro Trp Leu Ala Phe Pro Lys Ser Val Phe Asn Asn Leu Gly Gln Tyr
 165 170 175

 Phe Asn Gln Glu Lys Met Arg Leu Ala Phe Cys Phe Gln Ser Lys Tyr
 180 185 190

 Leu Gly Met Ser Pro Trp Glu Cys Pro Ala Leu Phe Thr Met Leu Pro
 195 200 205

 Tyr Leu Glu His Glu Tyr Gly Ile Tyr His Val Lys Gly Gly Leu Asn
 210 215 220

 Arg Ile Ala Ala Ala Met Ala Gln Val Ile Ala Glu Asn Gly Gly Glu
 225 230 235 240

 Ile His Leu Asn Ser Glu Ile Glu Ser Leu Ile Ile Glu Asn Gly Ala
 245 250 255

 Ala Lys Gly Val Lys Leu Gln His Gly Ala Glu Leu Arg Gly Asp Glu
 260 265 270

 Val Ile Ile Asn Ala Asp Phe Ala His Ala Met Thr His Leu Val Lys
 275 280 285

 Pro Gly Val Leu Lys Lys Tyr Thr Pro Glu Asn Leu Lys Gln Arg Glu
 290 295 300

 Tyr Ser Cys Ser Thr Phe Met Leu Tyr Leu Gly Leu Asp Lys Ile Tyr
 305 310 315 320

 Asp Leu Pro His His Thr Ile Val Phe Ala Lys Asp Tyr Thr Thr Asn
 325 330 335

 Ile Arg Asn Ile Phe Asp Asn Lys Thr Leu Thr Asp Asp Phe Ser Phe
 340 345 350

Tyr Val Gln Asn Ala Ser Ala Ser Asp Asp Ser Leu Ala Pro Ala Gly
 355 360 365
 Lys Ser Ala Leu Tyr Val Leu Val Pro Met Pro Asn Asn Asp Ser Gly
 370 375 380
 Leu Asp Trp Gln Ala His Cys Gln Asn Val Arg Glu Gln Val Leu Asp
 385 390 395 400
 Thr Leu Gly Ala Arg Leu Gly Leu Ser Asp Ile Arg Ala His Ile Glu
 405 410 415
 Cys Glu Lys Ile Ile Thr Pro Gln Thr Trp Glu Thr Asp Glu His Val
 420 425 430
 Tyr Lys Gly Ala Thr Phe Ser Leu Ser His Lys Phe Ser Gln Met Leu
 435 440 445
 Tyr Trp Arg Pro His Asn Arg Phe Glu Glu Leu Ala Asn Cys Tyr Leu
 450 455 460
 Val Gly Gly Gly Thr His Pro Gly Ser Gly Leu Pro Thr Ile Tyr Glu
 465 470 475 480
 Ser Ala Arg Ile Ser Ala Lys Leu Ile Ser Gln Lys His Arg Val Arg
 485 490 495
 Phe Lys Asp Ile Ala His Ser Ala Trp Leu Lys Lys Ala Lys Ala
 500 505 510

<210> 77
 <211> 1491
 <212> DNA
 <213> Methyloimonas 16a

<220>
 <223> CRTN2

<400> 77
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 gtcggcgca agtcaacat catgacccaa gacggctta cttcgatct gggccgtcc 180
 attttgcgca tgccgcacat ctttgaggcc ttgttcacag gggccggcaa aaacatggcc 240
 gattacgtgc aaatccagaa agtcgaaccg cactggcgca atttcttcga ggacggtagc 300
 gtgatcgact tggcgaaga cgccgaaacc cagcgcccg agctggataa acttggcccc 360
 ggcacttacg cgcaattcca ggcgtttctg gactattcga aaaacctctg cacggaaaacc 420
 gaagccggtt acttcgccaa gggcctggac ggcttttggg atttactcaa gttttacggc 480
 ccgctccgca gcctgctgag tttcgacgtc ttccgcagca tggaccaggc cgtgcgcgc 540
 tttatcccg atcccaagtt ggtcgaatac ctgaattact tcataaaaaa cgtcggtcc 600
 tcgccttacg atgcgcccgc cttgatgaac ctgctgcctt acattcaata tcattacggc 660
 ctgtggtaacg tgaaaggcgg catgtatggc atggcgcagg ccatggaaaa actggccgtg 720
 gaattggcgg tcgagattcg tttagatgcc gaggtgtcgg aaatccaaaa acaggacggc 780
 agagcctcgcc cgtaaaagtt ggcgaacggc gacgtgtcgc cggccgacat cgtgggtcg 840
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 aaaaatgcaggc gcttcgagcc tagctgtcc ggcctggc tgcaatttggg cgtggacagg 960
 ctgtatccgc aactggcgca ccacaatttc ttttattccg atcatcccg cgaacatttc 1020
 gatgcggtat tcaaaagcca tcgcctgtcg gacgatccga ccatttatcc ggtcgcccg 1080
 tgcaagaccg accccgcccc ggcgcggcc ggctgcgaga tcatcaaat cctgccccat 1140
 atcccgacc tgcaccccgaa caaactgctg accggccgagg attattcagc cttgcgcgag 1200

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cggtgtctgg tcaaactcg aacgcattggc ctgacggatt tacgccaaca catcgtgacc 1260
gaagaatact ggacccgcg gatattcag gccaaatatt attcaaacc gggctcgatt 1320
tacggcgtgg tcggcggacc cttcaaaaac ctgggttca aggcaccta acgcagcagc 1380
gaattatcca atctgtattt cgtcggcgcc agcgtcaatc ccggcgccgg catgccatg 1440
gtgacgctgt cccggcaatt ggtgaggac aagattgtgg cggatttgca a 1491

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<210> 78
<211> 497
<212> PRT
<213> *Methylomonas* 16a

<220>
<223> Amino acid sequences encoded by CRTN2

<400> 78
Met Asn Ser Asn Asp Asn Gln Arg Val Ile Val Ile Gly Ala Gly Leu
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Gly Gly Leu Ser Ala Ala Ile Ser Leu Ala Thr Ala Gly Phe Ser Val
20 25 30

Gln Leu Ile Glu Lys Asn Asp Lys Val Gly Gly Lys Leu Asn Ile Met
35 40 45

Thr Lys Asp Gly Phe Thr Phe Asp Leu Gly Pro Ser Ile Leu Thr Met
50 55 60

Pro His Ile Phe Glu Ala Leu Phe Thr Gly Ala Gly Lys Asn Met ala
65 70 75 80

Asp Tyr Val Gln Ile Gln Lys Val Glu Pro His Trp Arg Asn Phe Phe
85 90 95

Glu Asp Gly Ser Val Ile Asp Leu Cys Glu Asp Ala Glu Thr Gln Arg
 100 105 110

Arg Glu Leu Asp Lys Leu Gly Pro Gly Thr Tyr Ala Gln Phe Gln Arg
115 120 125

Phe	Leu	Asp	Tyr	Ser	Lys	Asn	Leu	Cys	Thr	Glu	Thr	Glu	Ala	Gly	Tyr
130						135						140			

Phe Ala Lys Gly Leu Asp Gly Phe Trp Asp Leu Leu Lys Phe Tyr Gly
145 150 155 160

Pro Leu Arg Ser Leu Leu Ser Phe Asp Val Phe Arg Ser Met Asp Gln
165 170 175

Gly Val Arg Arg Phe Ile Ser Asp Pro Lys Leu Val Glu Ile Leu Asn
180 185 190

Tyr Phe Ile Lys Tyr Val Gly Ser Ser Pro Tyr Asp Ala Pro Ala Leu
195 200 205

Met	Asn	Leu	Leu	Pro	Tyr	Ile	Gln	Tyr	His	Tyr	Gly	Leu	Trp	Tyr	Val
210						215						220			

Lys Gly Gly Met Tyr Gly Met Ala Gln Ala Met Glu Lys Leu Ala Val
 225 230 235 240

Glu Leu Gly Val Glu Ile Arg Leu Asp Ala Glu Val Ser Glu Ile Gln
 245 250 255

 Lys Gln Asp Gly Arg Ala Cys Ala Val Lys Leu Ala Asn Gly Asp Val
 260 265 270

 Leu Pro Ala Asp Ile Val Val Ser Asn Met Glu Val Ile Pro Ala Met
 275 280 285

 Glu Lys Leu Leu Arg Ser Pro Ala Ser Glu Leu Lys Lys Met Gln Arg
 290 295 300

 Phe Glu Pro Ser Cys Ser Gly Leu Val Leu His Leu Gly Val Asp Arg
 305 310 315 320

 Leu Tyr Pro Gln Leu Ala His His Asn Phe Phe Tyr Ser Asp His Pro
 325 330 335

 Arg Glu His Phe Asp Ala Val Phe Lys Ser His Arg Leu Ser Asp Asp
 340 345 350

 Pro Thr Ile Tyr Leu Val Ala Pro Cys Lys Thr Asp Pro Ala Gln Ala
 355 360 365

 Pro Ala Gly Cys Glu Ile Ile Lys Ile Leu Pro His Ile Pro His Leu
 370 375 380

 Asp Pro Asp Lys Leu Leu Thr Ala Glu Asp Tyr Ser Ala Leu Arg Glu
 385 390 395 400

 Arg Val Leu Val Lys Leu Glu Arg Met Gly Leu Thr Asp Leu Arg Gln
 405 410 415

 His Ile Val Thr Glu Glu Tyr Trp Thr Pro Leu Asp Ile Gln Ala Lys
 420 425 430

 Tyr Tyr Ser Asn Gln Gly Ser Ile Tyr Gly Val Val Ala Asp Arg Phe
 435 440 445

 Lys Asn Leu Gly Phe Lys Ala Pro Gln Arg Ser Ser Glu Leu Ser Asn
 450 455 460

 Leu Tyr Phe Val Gly Gly Ser Val Asn Pro Gly Gly Gly Met Pro Met
 465 470 475 480

 Val Thr Leu Ser Gly Gln Leu Val Arg Asp Lys Ile Val Ala Asp Leu
 485 490 495

Gln
497

<210> 79
 <211> 1455
 <212> DNA
 <213> METHYLOMONAS SP.

<400> 79

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attgaagatt tgagaaaaat gacggctggc atgacttgca gtagattgcc agaagatctt 180
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gttactactc tgactggcca aacgatcgc ctcgaagact acgcgcgttca 780
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gctggcgaca aaaaagttagc catgatctt ggttgcgtt ctctgggtt cgttgcgtt 960
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atcccaacct tcata 1455

<210> 80

<211> 485

<212> PRT

<213> METHYLOMONAS SP.

<400> 80

Arg Arg Cys Ser Cys Ile Ser Val Leu Leu Arg Leu Arg Phe Tyr His
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His Leu Leu Leu Val Ala Leu Leu Arg Pro Leu Val Leu Lys Asn Arg
20 25 30

Leu His Arg Arg Cys Phe Leu Ile Glu Asp Leu Arg Lys Met Thr
35 40 45

Ala Gly Met Thr Cys Ser Arg Leu Pro Glu Asp Leu Asn Tyr Lys Phe
50 55 60

Ser Ser Asn Arg Gly Gly Asn Met Lys Ile Ile Lys Asp Arg Val Ala
65 70 75 80

Lys Leu Ser Phe Val Ala Leu Leu Ile Thr Met Thr Ala Ala Met Phe
85 90 95

Tyr Ala Pro Thr Ala Ser Ala His Gly Glu Lys Ser Gln Ala Ala Phe
100 105 110

Met Arg Met Arg Thr Ile His Trp Phe Asp Leu Asn Trp Ser Ala Asp
115 120 125

Glu Val Ala Val Asn Asp Thr Met Thr Ile Ser Gly Lys Phe His Val
130 135 140

Phe Ala Gly Trp Pro Glu Thr Val Asp Lys Pro Glu Val Ser Phe Leu
 145 150 155 160
 Asn Ile Gly Ile Pro Gly Pro Val Phe Ile Arg Ala Gly Ser Trp Ile
 165 170 175
 Gly Gly Gln Leu Val Pro Arg Ser Val Ser Leu Glu Leu Gly Glu Thr
 180 185 190
 Tyr Glu Phe Lys Val Leu Leu Lys Ala Arg Arg Pro Gly Asp Trp His
 195 200 205
 Val His Thr Met Met Asn Val Gln Gly Gly Pro Ile Ile Gly Pro
 210 215 220
 Gly Lys Trp Val Thr Ile Thr Gly Lys Met Ser Asp Phe Val Asn Pro
 225 230 235 240
 Val Thr Thr Leu Thr Gly Gln Thr Ile Asp Leu Glu Asp Tyr Ala Leu
 245 250 255
 Asp Asn Val Tyr Phe Trp His Ala Val Trp Phe Ala Ile Gly Phe Ala
 260 265 270
 Trp Leu Ile Phe Trp Ile Lys Arg Pro Ile Phe Val Pro Arg His Ile
 275 280 285
 Ala Val Ser Thr Gly Lys Ala Asp Ser Leu Ile Ser Ala Gly Asp Lys
 290 295 300
 Lys Val Ala Met Ile Phe Gly Val Gly Thr Leu Val Ile Val Ala Ala
 305 310 315 320
 Ser Met Gly Ala Thr Asn Glu Lys Tyr Pro Val Thr Thr Pro Leu Gln
 325 330 335
 Ala Gly Leu Leu Arg Gly Met Lys Pro Tyr Gln Met Pro Glu Ser Thr
 340 345 350
 Val Ser Val Lys Val Asp Asp Ala Thr Tyr Arg Val Pro Gly Arg Ala
 355 360 365
 Met Gln Met Thr Leu Thr Ile Thr Asn Asn Gly Asp Ser Ala Val Arg
 370 375 380
 Leu Gly Glu Phe Asn Thr Ala Gly Val Arg Phe Leu Asp Ser Ser Val
 385 390 395 400
 His Glu Asp Glu Thr Gly Tyr Pro Asp Asp Leu Leu Ala Glu Asp Gly
 405 410 415
 Leu Ser Val Ser Asp Asn Ser Pro Ile Ala Pro Gly Glu Thr Arg Thr
 420 425 430
 Val Glu Val Thr Ala Ser Asp Ala Ala Trp Glu Val Tyr Arg Leu Ala
 435 440 445
 Asp Leu Ile Tyr Asp Pro Asp Ser Arg Phe Ala Gly Leu Met Phe Phe
 450 455 460

Trp Asp Glu Asn Gly Asn Arg Gln Met Thr Met Val Asp Ala Pro Leu
465 470 475 480

Ile Pro Thr Phe Ile
485

<210> 81
<211> 1429
<212> DNA
<213> METHYLOMONAS SP.

<400> 81

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gctaataccg	catacgtct	acggaggaaa	gccggggacc	ttcgggcctg	gcgctaata	180
atgagcctat	gtcggtttag	ctagttggtg	gggttaaaggc	ctaccaaggc	gacgatccgt	240
agctggctcg	agaggatgat	cagccacact	gggactgaga	cacggcccag	actcctacgg	300
gagggcagcag	tggggaatat	tggacaatgg	gcgcaagcct	gatccagcaa	taccgcgtgt	360
gtgaagaagg	cctgggggtt	gtaaagcact	ttcaatggga	aggaacacct	atcggttaat	420
acccggtaga	ctgacattac	ccatacaaga	agcaccggct	aactccgtgc	cagcagccgc	480
ggtaatacgg	agggtgcaag	cgttaatcg	aattactggg	cgtaaagcgt	gcgttaggcgg	540
tttttaagt	cagatgtgaa	agccctggc	ttaacctggg	aactgcattt	gatactgggg	600
aactagagtt	gagtagagga	gagtggaaatt	tcaggtgtag	cggtaaatg	cgtagagatc	660
tgaaggaaaca	ccagtggcga	aggcggtct	ctggactcaa	actgacgctg	aggtacgaaa	720
gcgtgggtag	caaacaggat	tagataccct	ggtagtccac	gccgttaaacg	atgtcaacta	780
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ctcggtcg	gagatgttgg	gttaagtccc	gtaacgagcg	caacccttat	ccttagttgc	1080
cagcgcgtca	tggcggaac	tctaggaga	ctgcccgtga	taaaccggag	gaaggtgggg	1140
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acagagggtt	gcgaactcgc	gagagccagc	caatccccaa	aagccgatcc	tagtccggat	1260
tgcagtctgc	aactcgactt	gcatgaagtc	ggaatcgcta	gtaatcgccg	atcagaatgc	1320
cgcggtaat	acgttcccgg	gccttgtaca	caccggccgt	cacaccatgg	gagtgggtt	1380
aaaaagaagt	agtagttt	accttcggga	gggcgttac	cacttgcgt		1429